

**Kemmerer, Elizabeth**

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**From:** Kemmerer, Elizabeth  
**Sent:** Thursday, June 19, 2003 2:29 PM  
**To:** Kunz, Gary  
**Subject:** SPDI favor

**Importance:** High

Hi Gary-

I am currently working on 09/941992, a SPDI case which is a date case. The 2 companion cases are not yet docketed: 09/990711 and 09/991150. They're both in central files on the 12th floor. Can these be docketed to me as well, since it would be easy to write up the 3 cases together, and they're all date cases?

Thanks a bunch,

Elizabeth (Betsy) Kemmerer  
Art Unit 1646  
308-2673  
CM1-10B17  
Mailbox: 10D19

STIC-Biotech/ChemLib

97031

**From:** Kemmerer, Elizabeth  
**Sent:** Thursday, June 19, 2003 2:30 PM  
**To:** STIC-Biotech/ChemLib  
**Subject:** sequence search request

Please search SEQ ID NO: 20 for 09/941992; regular and interference, please.

Thanks,

Elizabeth (Betsy) Kemmerer  
Art Unit 1646  
308-2673  
CM1-10B17  
Mailbox: 10D19

CRBS

Mary Jane Kuhl  
Tech. Info. Specialist, STIC  
TC-1600  
CM-1, Room 6A-06  
Phone: 605-1155







XX Birse CE, Rosen CA;  
 XX WPI: 2002-122018/16.  
 DR N-PSDB; ABL90743.  
 XX Novel 1405 isolated polypeptides, useful for diagnosis, treatment and  
 PT prevention of neural, immune system, muscular, reproductive,  
 PT gastrointestinal, pulmonary, cardiovascular, renal and proliferative  
 PT disorders -  
 XX Claim 11: SEQ ID NO 2710; 208lpp + Sequence Listing; English.  
 XX The invention relates to novel genes (ABL9449-ABL90853) and proteins  
 CC (ABB9040-ABB9044) useful for preventing, treating or ameliorating  
 CC medical conditions e.g. by protein or gene therapy. The genes are  
 CC isolated from a range of human tissues disclosed in the specification.  
 CC The nucleic acids, proteins, antibodies and (ant)agonists are useful  
 CC in the diagnosis, treatment and prevention of: (a) cancer, e.g. breast  
 CC and ovarian cancer and other cancers of the adrenal gland, bone, bone  
 CC marrow, breast, gastrointestinal tract, liver, lung, or urogenital;  
 CC (b) immune disorders e.g. Addison's disease, allergies, autoimmune  
 CC haemolytic anaemia, autoimmune thyroiditis, diabetes mellitus, Crohn's  
 CC disease, multiple sclerosis, rheumatoid arthritis and ulcerative  
 CC colitis; (c) cardiovascular disorders such as myocardial ischaemias;  
 CC (d) wound healing; (e) neurological diseases e.g. cerebral anoxia and  
 CC epilepsy; and (f) infectious diseases such as viral, bacterial, fungal  
 CC and parasitic infections.  
 CC Note: The sequence data for this patent did not form part of the  
 CC printed specification, but was obtained in electronic format directly  
 CC from WIPO at ftp.wipo.int/pub/published\_pct\_sequences.  
 XX  
 XX Sequence 530 AA;  
 \* Query Match 76.2%; Score 1816; DB 23; Length 530;  
 Best Local Similarity 94.3%; Pred. No. 3.8e-163;  
 Matches 362; Conservative 5; Mismatches 5; Indels 12; Gaps 2;  
 Qy 75 TCFHVV----PYSALTME-----ISTEQTERDSATAYRMVTEVLTGTLTAIQGIVG 134  
 Db 159 TCFHVV----PYSALTME-----ISTEQTERDSATAYRMVTEVLTGTLTAIQGIVG 206  
 Qy 135 QADTPCFQDNSTVSQSANHHTGTTSHRETQKAYLLAAGVIVCIICAVILILGVRE 194  
 Db 207 QADTPCFQDLNSSTVSQSANHHTGTTSHRETQKAYLLAAGVIVCIICAVILILGVRE 266  
 Qy 195 QREPYEAQOSEPTAYFRGLRLVMSHGPIYKLTGFLFTSLAFMLVEGNFVLCYTLGFR 254  
 Db 267 QREPYEAQOSEPTAYFRGLRLVMSHGPIYKLTGFLFTSLAFMLVEGNFVLCYTLGFR 326  
 Qy 255 NEFQNLALLMLSATLTIPIWQWFLTRFGKKTAVYVGISSAVPFLILVALMESNLITYA 314  
 Db 327 NEFQNLALLMLSATLTIPIWQWFLTRFGKKTAVYVGISSAVPFLILVALMESNLITYA 386  
 Qy 315 VAVAAGISVAFAALLPWSMLPDVIDDFHLKQPHFGHTGTEPIFFSFYVFFTFKFSVSLGIS 374  
 Db 387 VAVAAGISVAFAALLPWSMLPDVIDDFHLKQPHFGHTGTEPIFFSFYVFFTFKFSVSLGIS 446  
 Qy 375 TSLDFAGYQTRGCSQPERVKFTLNMLVTNAPVILVLLGLLFLKMPIDERRRQNKAL 434  
 Db 447 TSLDFAGYQTRGCSQPERVKFTLNMLVTNAPVILVLLGLLFLKMPIDERRRQNKAL 506  
 Qy 435 QALRDEASSSGCSETDSTELASIL 458  
 Db 507 QALRDEASSSGCSETDSTELASIL 530  
 RESULT 8  
 AAB94114  
 ID AAB94114 standard; Protein: 365 AA.  
 XX  
 AC AAB94114;  
 XX

DT 26-JUN-2001 (first entry)  
 XX Human protein sequence SEQ ID NO:14354.  
 XX Human; primer; detection; diagnosis; antisense therapy; gene therapy.  
 XX Homo sapiens.  
 OS EP1074617-A2.  
 PN 07-FEB-2001.  
 PD 28-JUL-2000; 2000EP-0116126.  
 PF 29-JUL-1999; 99JP-0248036.  
 PR 27-AUG-1999; 99JP-0300253.  
 PR 11-JAN-2000; 2000JP-0118776.  
 PR 02-MAY-2000; 2000JP-0183767.  
 PR 09-JUN-2000; 2000JP-0241899.  
 XX (HELI-) HELIX RES INST.  
 XX Ota T, Isozaki T, Nishikawa T, Hayashi K, Saito K, Yamamoto J;  
 PI Ishii S, Sugiyama T, Wakamatsu A, Nagai K, Otsuki T;  
 XX WPI: 2001-318749/34.  
 DR Primer sets for synthesizing polynucleotides, particularly the 5602  
 XX full-length cDNAs defined in the specification, and for the detection  
 PT and/or diagnosis of the abnormality of the proteins encoded by the  
 PT full-length cDNAs -  
 XX Claim 8; SEQ ID 14354; 2537pp + CD ROM; English.  
 XX The present invention describes primer sets for synthesising 5602  
 CC full-length cDNAs defined in the specification. Where a primer set  
 CC comprises: (a) an oligo-dr primer and an oligonucleotide complementary  
 CC to the complementary strand of a polynucleotide which comprises one of  
 CC the 5602 nucleotide sequences defined in the specification, where the  
 CC oligonucleotide comprises at least 15 nucleotides; or (b) a combination  
 CC of an oligonucleotide comprising a sequence complementary to the  
 CC complementary strand of a polynucleotide which comprises a 5'-end  
 CC sequence and an oligonucleotide comprising a sequence complementary to a  
 CC polynucleotide which comprises a 3'-end sequence, where the  
 CC oligonucleotide comprises at least 15 nucleotides and the combination of  
 CC the 5'-end sequence/3'-end sequence is selected from those defined in  
 CC the specification. The primer sets can be used in antisense therapy and  
 CC in gene therapy. The primers are useful for synthesising polynucleotides,  
 CC particularly full-length cDNAs. The primers are also useful for the  
 CC detection and/or diagnosis of the abnormality of the proteins encoded by  
 CC the full-length cDNAs. The primers allow obtaining of the full-length  
 CC cDNAs easily without any specialised methods. AAH03166 to AAH13628 and  
 CC AAH13633 to AAH18742 represent human cDNA sequences; AAB92446 to  
 CC AAB95893 represent human amino acid sequences; and AAH13629 to AAH13632  
 CC represent oligonucleotides, all of which are used in the exemplification  
 CC of the present invention.  
 XX Sequence 365 AA;  
 Qy Query Match 41.5%; Score 990; DB 22; Length 365;  
 Best Local Similarity 90.0%; Pred. No. 3.8e-85;  
 Matches 197; Conservative 5; Mismatches 5; Indels 12; Gaps 2;  
 Qy 75 TCFHVV----PYSALTME-----ISTEQTERDSATAYRMVTEVLTGTLTAIQGIVG 134  
 Db 159 TCFHVV----PYSALTME-----ISTEQTERDSATAYRMVTEVLTGTLTAIQGIVG 206  
 Qy 135 QADTPCFQDNSTVSQSANHHTGTTSHRETQKAYLLAAGVIVCIICAVILILGVRE 194  
 Db 207 QADTPCFQDLNSSTVSQSANHHTGTTSHRETQKAYLLAAGVIVCIICAVILILGVRE 266  
 Qy 195 QREPYEAQOSEPTAYFRGLRLVMSHGPIYKLTGFLFTSLAFMLVEGNFVLCYTLGFR 254

KW corneal graft neovascularisation; neurological disorder; regeneration;  
 KW Huntington's chorea; Alzheimer's disease; Parkinson's disease;  
 KW infectious disease; chemotaxis.  
 OS Homo sapiens.  
 XX WO200076530-A1.  
 XX 21-DEC-2000.  
 XX 01-JUN-2000; 2000WO-US14933.  
 XX 11-JUN-1999; 99US-0138572.  
 XX (HUMA-) HUMAN GENOME SCI INC.  
 XX (ROSE/) ROSEN C A.  
 XX Rosen CA, Ruben SM, Komatsoulis GA;  
 XX WPI; 2001-071147/08.  
 XX N-PSDB; AAF33221.  
 XX Nucleic acids encoding 49 human secreted polypeptides, useful for  
 PT preventing, diagnosing and/or treating e.g. cancers, Parkinson's  
 PT disease and diabetic retinopathy -  
 XX Claim 11; Page 488; 554pp; English.  
 XX The polynucleotide sequences given in AAF33213 to AAF33261 encode the  
 CC human secreted proteins given in AAB64882 to AAB64930. AAB64931 to  
 CC AAB64991 represent human secreted polypeptide sequences and proteins  
 CC homologous to them, which are given in the exemplification of the present  
 CC invention. Human secreted proteins have activities based on the tissues  
 CC and cells the genes are expressed in. Examples of activities include:  
 CC immunomodulatory; antisclerotic; dermatological; immunosuppressive;  
 CC antiinflammatory; anti-HIV; immunostimulant; cytostatic; cardiac;  
 CC vascular; antimicrobial; anti-angiogenic; ophthalmological;  
 CC neuroprotectant; anticonvulsant; nootropic; antialzheimers;  
 CC antiparkinsonian; and vulnerary. The polynucleotides and polypeptides can  
 CC be used in the prevention, diagnosis and treatment of diseases associated  
 CC with inappropriate polypeptide expression. Disorders that may be  
 CC prevented, diagnosed and/or treated by the above methods include immune  
 CC disorders (e.g. multiple sclerosis, systemic lupus erythematosus and  
 CC human immuno-deficiency virus (HIV) infections), hyperproliferative  
 CC disorders (e.g. cancers and Gaucher's disease), cardiovascular diseases  
 CC (e.g. Scimitar syndrome, Chaga's cardiomyopathy and coronary  
 CC arteriosclerosis), angiogenic disorders (e.g. corneal graft  
 CC neovascularisation and diabetic retinopathy), neurological disorders  
 CC (e.g. Huntington's chorea, Alzheimer's disease and Parkinson's disease),  
 CC infectious diseases and/or for promoting wound healing, regeneration and  
 CC /or chemotaxis. AAF33204 to AAF33212 and AAB64881 represent sequences  
 CC used in the exemplification of the present invention.  
 XX Sequence 60 AA;  
 SQ Query Match 11.9%; Score 284; DB 22; Length 60;  
 Best Local Similarity 100.0%; Pred. No. 2.5e-19;  
 Matches 59; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 400 MLVTMAPIVLILGLLFLKMPIDERRRQNKALQALRDPASSGSGSETDSTELASTL 458  
 Db 1 MLVTMAPIVLILGLLFLKMPIDERRRQNKALQALRDPASSGSGSETDSTELASTL 59  
 RESULT 11  
 AAB64947  
 ID AAB64947 standard; Protein; 173 AA.  
 XX AAB64947;  
 AC AAB64947;  
 XX 23-MAR-2001 (first entry)  
 DT Human secreted protein sequence encoded by gene 9 SEQ ID NO:125.  
 DE

XX Human; secreted protein; diagnosis; immunomodulatory; antisclerotic;  
 KW dermatological; immunosuppressive; antiinflammatory; anti-HIV;  
 KW immunostimulant; cytostatic; cardiac; vascular; anti-angiogenic;  
 KW ophthalmological; neuroprotectant; nootropic; anticonvulsant; vulnerary;  
 KW antialzheimers; antiparkinsonian; antimicrobial; immune disorder;  
 KW multiple sclerosis; systemic lupus erythematosus; HIV; infection;  
 KW hyperproliferative disorder; cancer; Gaucher's disease; wound healing;  
 KW cardiovascular disease; Scimitar syndrome; Chaga's cardiomyopathy;  
 KW coronary arteriosclerosis; angiogenic disorder; diabetic retinopathy;  
 KW corneal graft neovascularisation; neurological disorder; regeneration;  
 KW Huntington's chorea; Alzheimer's disease; Parkinson's disease;  
 KW infectious disease; chemotaxis.  
 XX Homo sapiens.  
 XX WO200076530-A1.  
 XX 21-DEC-2000.  
 XX 01-JUN-2000; 2000WO-US14933.  
 XX 11-JUN-1999; 99US-0138572.  
 XX (HUMA-) HUMAN GENOME SCI INC.  
 XX (ROSE/) ROSEN C A.  
 XX Rosen CA, Ruben SM, Komatsoulis GA;  
 XX WPI; 2001-071147/08.  
 XX Nucleic acids encoding 49 human secreted polypeptides, useful for  
 PT preventing, diagnosing and/or treating e.g. cancers, Parkinson's  
 PT disease and diabetic retinopathy -  
 XX Claim 11; Page 525; 554pp; English.  
 XX The polynucleotide sequences given in AAF33213 to AAF33261 encode the  
 CC human secreted proteins given in AAB64882 to AAB64930. AAB64931 to  
 CC AAB64991 represent human secreted polypeptide sequences and proteins  
 CC homologous to them, which are given in the exemplification of the present  
 CC invention. Human secreted proteins have activities based on the tissues  
 CC and cells the genes are expressed in. Examples of activities include:  
 CC immunomodulatory; antisclerotic; dermatological; immunosuppressive;  
 CC antiinflammatory; anti-HIV; immunostimulant; cytostatic; cardiac;  
 CC vascular; antimicrobial; anti-angiogenic; ophthalmological;  
 CC neuroprotectant; anticonvulsant; nootropic; antialzheimers;  
 CC antiparkinsonian; and vulnerary. The polynucleotides and polypeptides can  
 CC be used in the prevention, diagnosis and treatment of diseases associated  
 CC with inappropriate polypeptide expression. Disorders that may be  
 CC prevented, diagnosed and/or treated by the above methods include immune  
 CC disorders (e.g. multiple sclerosis, systemic lupus erythematosus and  
 CC human immuno-deficiency virus (HIV) infections), hyperproliferative  
 CC disorders (e.g. cancers and Gaucher's disease), cardiovascular diseases  
 CC (e.g. Scimitar syndrome, Chaga's cardiomyopathy and coronary  
 CC arteriosclerosis), angiogenic disorders (e.g. corneal graft  
 CC neovascularisation and diabetic retinopathy), neurological disorders  
 CC (e.g. Huntington's chorea, Alzheimer's disease and Parkinson's disease),  
 CC infectious diseases and/or for promoting wound healing, regeneration and  
 CC /or chemotaxis. AAF33204 to AAF33212 and AAB64881 represent sequences  
 CC used in the exemplification of the present invention.  
 XX Sequence 173 AA;  
 SQ Query Match 8.2%; Score 195; DB 22; Length 173;  
 Best Local Similarity 66.2%; Pred. No. 2.7e-10;  
 Matches 43; Conservative 5; Mismatches 5; Indels 12; Gaps 2;  
 QY 75 TCFSIASLKOWSRVSMPEPTLSPCSSATEQTERDSATAYRMTVEVLGTVLGTATGQIVG 134  
 Db 121 TCFHV----PYSALTMF-----ISTEQTERDSATAYRMTVEVLGTVLGTATGQIVG 168  
 QY 135 QADTP 139



GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: June 19, 2003, 17:46:17 ; Search time 26 seconds  
(without alignments)  
518.296 Million cell updates/sec

Title: US-09-941-992-20

Perfect score: 2384

Sequence: 1 MWLRWALSPLPSSCLWAEPG.....DEASSSGCSETDSTELASIL 458

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents\_AA.\*

- 1: /cgn2\_6/ptodata/1/iaa/5A\_COMB.pep.\*
- 2: /cgn2\_6/ptodata/1/iaa/5B\_COMB.pep.\*
- 3: /cgn2\_6/ptodata/1/iaa/6A\_COMB.pep.\*
- 4: /cgn2\_6/ptodata/1/iaa/6B\_COMB.pep.\*
- 5: /cgn2\_6/ptodata/1/iaa/PCFUS\_COMB.pep.\*
- 6: /cgn2\_6/ptodata/1/iaa/backfiles1.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	143.5	6.0	457	2	US-08-882-704A-6
2	143.5	6.0	457	4	US-09-151-957-6
3	128.5	5.4	456	6	5432081-7
4	120.5	5.1	428	6	5432081-9
5	109	4.6	457	3	US-09-416-213-2
6	109	4.6	457	4	US-09-416-214-2
7	109	4.6	457	4	US-09-035-676-2
8	107.5	4.5	1280	2	US-08-752-447-2
9	107.5	4.5	1280	4	US-09-316-167-2
10	107	4.5	426	6	5268463-8
11	106.5	4.5	1280	2	US-08-583-276-19
12	106.5	4.5	1280	6	5206352-4
13	106	4.4	580	2	US-08-677-049-12
14	103	4.3	457	6	5268463-7
15	101	4.2	460	1	US-08-689-974-5
16	101	4.2	460	3	US-09-058-376-5
17	97.5	4.1	822	4	US-08-684-932A-38
18	96.5	4.0	364	5	PCT-US96-10618-2
19	96	4.0	1279	2	US-08-784-649A-2
20	95.5	4.0	445	4	US-09-134-001C-3507
21	95	4.0	435	6	5268463-9
22	95	4.0	436	6	5432081-10
23	94.5	4.0	290	4	US-09-134-001C-4893
24	93.5	3.9	369	4	US-09-172-353-6
25	93.5	3.9	384	4	US-09-200-673-15
26	93	3.9	808	4	US-09-134-001C-3105
27	92.5	3.9	383	3	US-09-045-186-2

28	92.5	3.9	384	1	US-08-232-144-4	Sequence 4, Appli
29	92.5	3.9	384	2	US-08-555-268A-15	Sequence 15, Appli
30	92.5	3.9	384	5	PCT-US93-05039-3	Sequence 3, Appli
31	92.5	3.9	765	2	US-08-846-762-5	Sequence 5, Appli
32	92	3.9	364	4	US-08-763-938-2	Sequence 2, Appli
33	91	3.8	640	4	US-09-627-376-16	Sequence 16, Appli
34	91	3.8	683	4	US-09-134-001C-5576	Sequence 5576, Ap
35	91	3.8	878	4	US-09-556-706B-2	Sequence 2, Appli
36	91	3.8	907	3	US-08-783-774-2	Sequence 1, Appli
37	91	3.8	907	4	US-09-328-599A-1	Sequence 1, Appli
38	91	3.8	907	5	PCT-US95-04611A-19	Sequence 19, Appli
39	89.5	3.8	404	1	US-08-696-770-2	Sequence 2, Appli
40	89.5	3.8	404	2	US-09-015-557-2	Sequence 2, Appli
41	89.5	3.8	540	4	US-09-513-057C-33	Sequence 33, Appli
42	88.5	3.7	462	2	US-08-898-976-2	Sequence 2, Appli
43	88.5	3.7	462	2	US-08-898-976-4	Sequence 4, Appli
44	88	3.7	382	1	US-08-415-818-7	Sequence 7, Appli
45	88	3.7	382	2	US-08-894-236-7	Sequence 7, Appli

## ALIGNMENTS

RESULT 1  
US-08-882-704A-6  
; Sequence 6, Application US/08882704A  
; Patent No. 5879906  
; GENERAL INFORMATION:  
; APPLICANT: Jefferson, Richard A.  
; APPLICANT: Wilson, Katherine J.  
; APPLICANT: Leader, Michael  
; TITLE OF INVENTION: GLUCURONIDE REPRESSORS AND USES THEREOF  
; NUMBER OF SEQUENCES: 19  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: SEED AND BERRY LLP  
; STREET: 6300 Columbia Center, 701 Fifth Avenue  
; CITY: Seattle  
; STATE: Washington  
; COUNTRY: USA  
; ZIP: 98104-7092  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/882,704A  
; FILING DATE: 25-JUN-1997  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: No. 5879906tenburg Ph.D., Carol  
; REGISTRATION NUMBER: 39,317  
; REFERENCE/DOCKET NUMBER: 190106.404  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (206) 622-4900  
; TELEFAX: (206) 682-6031  
; INFORMATION FOR SEQ ID NO: 6:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 457 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear

Query Match 6.0%; Score 143.5; DB 2; Length 457;  
Best Local Similarity 19.8%; Pred. No. 2.le-05;  
Matches 75; Conservative 62; Mismatches 178; Indels 63; Gaps 13;

Qy	73	IGTCFSTASLKQWRSVSMFPTRLSPCSSATQTERDSATAYRMTVEVLGTVLGTAIQOI	132
Db	119	LGLCYSLNIPYGSLATAMTQQ--PQSRARLGAARGAAS--LTFVCLAFILGPSIK---	171
Qy	133	VGQADTPCFQDFNSSTVASQSANHTGTTSHRETQKAYLLAAGVIVCIYIICAVILIGV	192

```

357 357 SYEYVFFTFKASGVSIGISTLSLDPAHQVQTRGCCSOPERVKETLNLMTVMPIVUILGLLL 416
Qy
364 364 SLFSETRCKGQAGISIPAFILGLSGYIANQVQTE-VINGIRTSIALVPCGFMLLAFVI 422
Db
417 417 FKMYPIDEERRRQ-----NKKALQ 435
Qy
423 423 IWFPYPLTDKKFKETIWEIDNRKKVQ 447
Db

```

## RESULT 4

```

5432081-9
; Patent No. 5432081
; APPLICANT: JEFFERSON, RICHARD A.
; TITLE OF INVENTION: HOST CELLS TRANSFORMED WITH THE E. COLI
; GLUCORONIDE PERMEASE GENE
; NUMBER OF SEQUENCES: 10
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/138,546
; FILING DATE: 15-OCT-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 447,976
; FILING DATE: 08-DEC-1989
; APPLICATION NUMBER: 264,586
; FILING DATE: 31-OCT-1988
; APPLICATION NUMBER: 119,102
; FILING DATE: 10-NOV-1987
; SEQ ID NO: 9:
; LENGTH: 428
5432081-9

```

[illegible]

## RESULT 5

```

US-09-416-213-2
; Sequence 2, Application US/09416213
; Patent No. 6110690
; GENERAL INFORMATION:
; APPLICANT: Goeddel, David V.
; APPLICANT: Jiang, Yingping
; TITLE OF INVENTION: Suppressors of Death Domains
; NUMBER OF SEQUENCES: 2
;
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94010
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:

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Db 111 MTRYAYYSIGAGVLAAYIQVSWCLAAAGROIHKIRKOFFHAIMRQEIQWDFVDHVG 170  
Qy 211 RGLRLV-----MSHGPKIKLITGLFTSLAFMLVEGNFVLCFTYTLGFRNEFQNLAIM 265  
Db 171 LNRLTDDVKINEGIDKI--GMFFOSMA-----TFTGFIQVFTRGWKLTLVILA 220  
Qy 266 LSAT--LTIPIWQWFLTRFGKKTAVYVGISSAVPFLILVAL----- 304  
Db 221 ISPLGLSAVAKILSSFTDKELLAYAKAGAAVEVLAIRIVIAFGGOKKELERYKN 280  
Qy 305 MESNLIITYAVAAAGISVAAAFLLPWSMLPDVIDDFHLKOPHFGHTEPIFFSFY----- 359  
Db 281 LLEAKRIGIKAITANISIGAAFLLIYASVAVF-----WYGTTLVLSGEYSIGQV 331  
Qy 360 --VFETKFSVSLGISTLSLDF-----AGYQ-----TRGCSOPERVKFT 397  
Db 332 LTVEFSLVIGAFSVGOASPSIEAFANARGAAEYEIFKIIDNKPSIDSYSKSGHKPDNIK-- 389  
Qy 398 LNMLVTMAPIVLILGLLLEK-----MYPIDEERRONKKALQALRDEAS--S 444  
Db 390 -----GNLEFRNVHFSYP-----SRKEVKILKGLNLKQVSGQTVVALVGN 429  
Qy 445 GCSETDSTEL 454  
Db 430 GCCKSTTVQL 439

RESULT 9  
US-09-316-167-2  
; Sequence 2, Application US/09316167  
; Patent No. 6365357  
; GENERAL INFORMATION:  
; APPLICANT: Mechtner, Eugene  
; APPLICANT: Roninson, Igor B  
; TITLE OF INVENTION: Methods and Reagents for Preparing and  
; TITLE OF INVENTION: Using Immunological Agents Specific for P-glycoprotein  
; NUMBER OF SEQUENCES: 2  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: McDonnell Boehnen Hulbert & Berghoff Ltd.  
; STREET: 300 South Wacker Drive, Seventh Floor  
; CITY: Chicago  
; STATE: Illinois  
; COUNTRY: USA  
; ZIP: 60606  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/316,167  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/752,447  
; FILING DATE: 15-NOV-1996  
; ATTORNEY/AGENT INFORMATION:  
; NAME: No. 6365357nan, Kevin E  
; REGISTRATION NUMBER: 35,303  
; REFERENCE/DOCKET NUMBER: 95,1121  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 312-913-0001  
; TELEFAX: 312-913-9808  
; INFORMATION FOR SEQ ID NO: 2:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 1280 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-09-316-167-2

Query Match 4.5%; Score 107.5; DB 4; Length 1280;  
Best Local Similarity 19.5%; Pred. No. 0.27;

Matches 84; Conservative 67; Mismatches 148; Indels 131; Gaps 19;  
Qy 115 MTEVEGLTVL---GTAIQGIVGQ-----ADTPCFQDFNSSTVASQSANHTGTTSHRE- 165  
Db 51 MVTGTLAAIIHAGLPLMLMLVFGEMTDIFANAGNLEDLMNITNRSINDTGFPMNLEED 110  
Qy 166 -TOKAYL---LAAGVIVICIVICAVILILGVRE---OREPYEAQQSEPIAYF----- 210  
Db 111 MTRYAYYSIGAGVLAAYIQVSWCLAAAGROIHKIRKOFFHAIMRQEIQWDFVDHVG 170  
Qy 211 RGLRLV-----MSHGPKIKLITGLFTSLAFMLVEGNFVLCFTYTLGFRNEFQNLAIM 265  
Db 171 LNRLTDDVKINEGIDKI--GMFFOSMA-----TFTGFIQVFTRGWKLTLVILA 220  
Qy 266 LSAT--LTIPIWQWFLTRFGKKTAVYVGISSAVPFLILVAL----- 304  
Db 221 ISPLGLSAVAKILSSFTDKELLAYAKAGAAVEVLAIRIVIAFGGOKKELERYKN 280  
Qy 305 MESNLIITYAVAAAGISVAAAFLLPWSMLPDVIDDFHLKOPHFGHTEPIFFSFY----- 359  
Db 281 LLEAKRIGIKAITANISIGAAFLLIYASVAVF-----WYGTTLVLSGEYSIGQV 331  
Qy 360 --VFETKFSVSLGISTLSLDF-----AGYQ-----TRGCSOPERVKFT 397  
Db 332 LTVEFSLVIGAFSVGOASPSIEAFANARGAAEYEIFKIIDNKPSIDSYSKSGHKPDNIK-- 389  
Qy 398 LNMLVTMAPIVLILGLLLEK-----MYPIDEERRONKKALQALRDEAS--S 444  
Db 390 -----GNLEFRNVHFSYP-----SRKEVKILKGLNLKQVSGQTVVALVGN 429  
Qy 445 GCSETDSTEL 454  
Db 430 GCCKSTTVQL 439

RESULT 10  
5268463-8  
; Patent No. 5268463  
; APPLICANT: JEFFERSON, RICHARD A.  
; TITLE OF INVENTION: PLAAAT PROMOTER a-GLUCURONIDASE GENE  
; CONSTRUCT  
; NUMBER OF SEQUENCES: 9  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/07/447,976  
; FILING DATE: 08-DEC-1989  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 119,102  
; FILING DATE: 10-NOV-1987  
; APPLICATION NUMBER: 264,586  
; FILING DATE: 31-OCT-1988  
; SEQ ID NO: 8  
; LENGTH: 426  
5268463-8

Query Match 4.5%; Score 107; DB 6; Length 426;  
Best Local Similarity 19.0%; Pred. No. 0.059;  
Matches 71; Conservative 59; Mismatches 169; Indels 74; Gaps 14;  
Qy 73 IGTCFSTASLQKQSRVSMFPTRLSPCSSATQETPRDSATAYMTVEVLTGVLTAIOGOI 132  
Db 111 LGLCYSLVNIPIYGSLATAMTQQ--PQSRARLGAARGIAAS--LTFVCLAFILIGPSIK--- 163  
Qy 133 VGOADTPCFQDFNSSTVASQSANHTGTTSHRETKAYLLAAGVIVICIVICAVILILGV 192  
Db 164 -----NSSPEEMVSVYH-----FWTIVLATAAGW--LYFIC-----PKST 196  
Qy 193 REQREPYEAQQSEPIAYFRLGLRLVMSHGPKIKLITGLFTSLAFMLVEGNFVLCFTYTLG 252  
Db 197 RENWVRIVAQPSLNIS---LQTLKRNRPFLMCLICIGALCVLISTFAVSASLFF---YVLN 249  
Qy 253 FRNEFQNLAIMLSATLTIPIW-----QWFLTRFGKKTAVYVGISSAVPFLILVAL 304  
Db 250 DTGLFTVLVL-----VQNPGWYCGIGTAGAXMVARIGKTKFLIGALLGTCGYLLFFWV 302

Qy 447 SETDSTEL 454  
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Db 432 GKSTTVQL 439

## RESULT 13

US-08-677-049-12  
; Sequence 12, Application US/08677049  
; Patent No. 5858707  
; GENERAL INFORMATION:  
; APPLICANT: Guimaraes, M. Jorge  
; APPLICANT: Bazan, J. Fernando  
; APPLICANT: McClanahan, Terrill K.  
; APPLICANT: Zlotnik, Albert  
; TITLE OF INVENTION: PURIFIED MAMMALIAN NUCLEOBASE PERMEASES;  
; TITLE OF INVENTION: NUCLEIC ACIDS; ANTIBODIES  
; NUMBER OF SEQUENCES: 12

; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: DNAX Research Institute  
; STREET: 901 California Avenue  
; CITY: Palo Alto  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94304-1104

; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/677.049  
; FILING DATE: 03-JUL-1996  
; CLASSIFICATION: 435

; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 60/000,788  
; FILING DATE: 03-JUL-1996  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Ching, Edwin P.

; REGISTRATION NUMBER: 34,090  
; REFERENCE/DOCKET NUMBER: DX0511  
; TELEPHONE: 415-852-9196  
; TELEFAX: 415-496-1200

; INFORMATION FOR SEQ ID NO: 12:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 580 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear

; MOLECULE TYPE: protein  
; FEATURE:  
; NAME/KEY: Region  
; LOCATION: 207..236

; OTHER INFORMATION: /note= "Encompasses TM 4 of Figure 4"  
; OTHER INFORMATION: /note= "Encompasses TM 9 and TM 10 of Figure 4"

; NAME/KEY: Region  
; LOCATION: 437..499  
; OTHER INFORMATION: /note= "Encompasses TM 9 and TM 10 of Figure 4"

; NAME/KEY: Region  
; LOCATION: 437..499  
; OTHER INFORMATION: /note= "Encompasses TM 9 and TM 10 of Figure 4"

; NAME/KEY: Region  
; LOCATION: 437..499  
; OTHER INFORMATION: /note= "Encompasses TM 9 and TM 10 of Figure 4"

; NAME/KEY: Region  
; LOCATION: 437..499  
; OTHER INFORMATION: /note= "Encompasses TM 9 and TM 10 of Figure 4"

; NAME/KEY: Region  
; LOCATION: 437..499  
; OTHER INFORMATION: /note= "Encompasses TM 9 and TM 10 of Figure 4"

; NAME/KEY: Region  
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; NAME/KEY: Region  
; LOCATION: 437..499  
; OTHER INFORMATION: /note= "Encompasses TM 9 and TM 10 of Figure 4"

; NAME/KEY: Region  
; LOCATION: 437..499  
; OTHER INFORMATION: /note= "Encompasses TM 9 and TM 10 of Figure 4"

Db 292 MKCAVIVGLVGCIVAAACGYDFRSGIDAAPVASFVWKTFTPLTIYAPLILPLAVMV 351  
Qy 100 SATQTERDSATAYRMTVEVLGTGLTAIOGIVGQADT-----PCQDENSS 147  
Db 352 IMMESIGDITATCDVSRLOVEGATFDSRIQGVGLNGITCLLAGLCTITPMSVFAQNGV 411  
Qy 148 TVASOSANHTHTTSHRETOKAYLLAAGVIVCIYIICAVILILGVREOREPEYEAQOSEPI 207  
Db 412 IALTPCANRRAG-----YCCCFLLVVMGI-----F 436  
Qy 208 AYFRGLRLVMSHGPIYIKLITGFLTSLAFMLVEGNFVLCFTYITGFRNEF-QNLLLAIML 266  
Db 437 AKF-AAALVAIPSSVLGGMTTFLFSSVAISGVR-----IMCSVDVTRNRRLTITASFAVGM 491  
Qy 267 SATLTIPIW-QWFLTRFGKKTAVVVGISSAVPELILVALMESNLIIITVAVAAAGISVAA 325  
Db 492 AATL-VPDWFSYFTYSGDNHAL-EGLLQAV-----ELVMANGFAVTGLGLLL 538  
Qy 326 AFLPLWSMLPDVID 339  
Db 539 NLILPEDMEEDVVE 552

## RESULT 14

5268463-7  
; Patent No. 5268463  
; APPLICANT: JEFFERSON, RICHARD A.  
; TITLE OF INVENTION: PLAANT PROMOTER a-GLUCURONIDASE GENE  
; CONSTRUCT  
; NUMBER OF SEQUENCES: 9  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/07/447,976  
; FILING DATE: 08-DEC-1989  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 119,102  
; FILING DATE: 10-NOV-1987  
; APPLICATION NUMBER: 264,586  
; FILING DATE: 31-OCT-1988  
; SEQ ID NO: 7:  
; LENGTH: 457  
5268463-7

Query Match 4.3%; Score 103; DB 6; Length 457;  
Best Local Similarity 18.9%; Pred. No. 0.16;  
Matches 74; Conservative 61; Mismatches 168; Indels 88; Gaps 16;  
Qy 73 IGTCFSTASLQKQSRVSMFPRLSPCSSATQTERDSATAYRMTVEVLGTGLTAIOGQI 132  
Db 118 LGLCYSLVNIPIYGLSATAMTQO--PNSRRLGAARGIAAS--LTFVCLAFILGPSIK--- 170  
Qy 133 VGQADTPCFQDFNSSTVASQSANTHTGTTSHRETOKAYLLAAGVIVCIYIICAVILILGV 192  
Db 171 -----NSSPEMVSVYHFV-----TIVLAIGWVLYYFC-----FKST 204  
Qy 193 REQREPEYEAQOSEPIAYFRGLRLVMSHGPIYIKLITGFLTSLAFMLVEGNFVLCFTYTLG 252  
Db 205 RENVVRIVAGPSLNIS---LQTLKRNRLPMLCIGALCVLISTFAVSASSLFVRY--- 257  
Qy 253 FRNEFQNLILAISATLTI---PIW-----QWFLTRFGKKTAVVVG-ISSAVPLI 300  
Db 258 -----LNDTGLPTVLVLVQNPWCYGGICTAGAXMVARIGKNTFLLIGALLGTCGYLL 309  
Qy 301 LVALMESNLIIITYAVAAAGISVAAAFLLPWSMLPDVIDDFHLQKPHFG-----TEP 353  
Db 310 FFWVSVSLPVALVALAIAISIGQGVTVTMWALADIVE-----YGEYLTGVRIEG 360  
Qy 354 IFFSYFFVFFKFAVSGVSLGISTLS---LDFAGYQTRGCSQPERKFTLMNLTMAPIVLI 410  
Db 361 LTVSLFSETRK--CGAIGGSSIPAFILGLSGYIANOVQTE-VIMGIRTSIALVPCGFM 417  
Qy 411 LLGULLPKMYPIDERRRQ-----NKKALQ 435  
Db 418 LLAFLVITWYPLTDKFKRETVEIDNRKKVQ 448



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: PRIOR APPLICATION NUMBER: 60/091544
: PRIOR FILING DATE: 1998-07-01
: PRIOR APPLICATION NUMBER: 60/091519
: PRIOR FILING DATE: 1998-07-02
: PRIOR APPLICATION NUMBER: 60/091626
: PRIOR FILING DATE: 1998-07-02
: PRIOR APPLICATION NUMBER: 60/091633
: PRIOR FILING DATE: 1998-07-02
: PRIOR APPLICATION NUMBER: 60/09178
: PRIOR FILING DATE: 1998-07-07
: PRIOR APPLICATION NUMBER: 60/091962
: PRIOR FILING DATE: 1998-07-07
: PRIOR APPLICATION NUMBER: 60/092182
: PRIOR FILING DATE: 1998-07-09

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Query Match 100.0%; Score 2384; DB 9; Length 458;

Query Match	100.00;	Score 2504;	DB 5;	Length 456;
Best Local Similarity	100.00;	Pred. No. 5.4e-185;		
Matches 458; Conservative	0;	Mismatches	0;	Indels 0;
Gaps	0;			

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Db	1	MWL	RWALS	LPSS	SCLWAB	PGMPS	OTPW	WAS	SAN	PNP	PG	PAW	ALCP	GSSS	PR	WP	SL	PT	SS	60																																		
QY	61	SGS	CTP	SH	TARP	IG	TCF	SIA	LK	QW	RS	VM	PT	PL	SP	CS	SAT	EQ	T	ER	DS	AT	AY	RM	VE	VL	120																											
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QY	301	L	V	A	M	E	S	N	L	I	T	Y	A	V	A	A	G	I	S	V	A	A	F	L	L	P	W	S	M	L	P	D	V	I	D	F	H	L	K	Q	P	H	F	H	G	T	E	P	I	F	S	F	V	360
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QY	361	F	T	F	K	S	A	S	G	I	S	T	S	L	D	F	A	G	Y	O	T	R	G	C	S	O	P	E	R	V	K	T	L	N	M	L	V	T	A	P	I	L	L	I	G	L	L	L	F	K	M	Y	420	
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## RESULT. T 2

US-09-989-293A-20  
; Sequence 20, Application US/09989293A  
; Patent No. US20020177164A1

GENERAL INFORMATION:

APPLICANT:	Ashkenazi, Avi J.
APPLICANT:	Baker, Kevin P.
APPLICANT:	Botstein, David
APPLICANT:	Desnoyers, Luc
APPLICANT:	Eaton, Dan L.
APPLICANT:	Ferrara, Napoleone
APPLICANT:	Fong, Sherman
APPLICANT:	Gerber, Hanspeter
APPLICANT:	Gerritsen, Mary E.
APPLICANT:	Goddard, Audrey
APPLICANT:	Godowski, Paul J.
APPLICANT:	Grimaldi, J. Christopher
APPLICANT:	Gurney, Austin L.
APPLICANT:	Kljavine, Ivar J.
APPLICANT:	Napier, Mary A.
APPLICANT:	Pan, James

## RESULT 3

US-09-989-735-20  
: Sequence 20, Application US/09989735  
: Publication No. US20020193299A1  
: GENERAL INFORMATION:  
: APPLICANT: Ashkenazi, Avi J.  
: APPLICANT: Baker, Kevin P.  
: APPLICANT: Botstein, David  
: APPLICANT: Desnoyers, Luc  
: APPLICANT: Eaton, Dan L.  
: APPLICANT: Ferrara, Napoleone  
: APPLICANT: Fong, Sherman  
: APPLICANT: Gerber, Hanspeter  
: APPLICANT: Gerritsen, Mary E.  
: APPLICANT: Goddard, Audrey  
: APPLICANT: Godowski, Paul J.  
: APPLICANT: Grimaldi, J. Christopher  
: APPLICANT: Gurney, Austin L.  
: APPLICANT: Kijavlin, Ivar J.  
: APPLICANT: Napier, Mary A.  
: APPLICANT: Pan, James  
: APPLICANT: Paoni, Nicholas F.  
: APPLICANT: Roy, Margaret Ann  
: APPLICANT: Stewart, Timothy A.  
: APPLICANT: Tumas, Daniel  
: APPLICANT: Watanabe, Colin K.  
: APPLICANT: Williams, P. Mickey  
: APPLICANT: Wood, William I.  
: APPLICANT: Zhang, Zemin  
: TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
: FILE REFERENCE: P2730P1C61  
: CURRENT APPLICATION NUMBER: US/09/989,735  
: CURRENT FILING DATE: 2001-11-19  
: PRIOR APPLICATION NUMBER: 60/049787  
: PRIOR FILING DATE: 1997-06-16  
: PRIOR APPLICATION NUMBER: 60/062250  
: PRIOR FILING DATE: 1997-10-17  
: PRIOR APPLICATION NUMBER: 60/065186  
: PRIOR FILING DATE: 1997-11-12  
: PRIOR APPLICATION NUMBER: 60/065311  
: PRIOR FILING DATE: 1997-11-13  
: PRIOR APPLICATION NUMBER: 60/066770  
: PRIOR FILING DATE: 1997-11-24  
: PRIOR APPLICATION NUMBER: 60/075945  
: PRIOR FILING DATE: 1998-02-25  
: PRIOR APPLICATION NUMBER: 60/078910  
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: PRIOR APPLICATION NUMBER: 60/083322  
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: PRIOR FILING DATE: 1998-06-22  
: PRIOR APPLICATION NUMBER: 60/090349  
: PRIOR FILING DATE: 1998-06-23

1	PRIOR FILING DATE: 1998-06-17	
2	PRIOR APPLICATION NUMBER: 60/089801	
3	PRIOR FILING DATE: 1998-06-18	
4	PRIOR APPLICATION NUMBER: 60/089907	
5	PRIOR FILING DATE: 1998-06-18	
6	PRIOR APPLICATION NUMBER: 60/089908	
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11	PRIOR FILING DATE: 1998-06-19	
12	PRIOR APPLICATION NUMBER: 60/089952	
13	PRIOR FILING DATE: 1998-06-19	
14	PRIOR APPLICATION NUMBER: 60/090246	
15	PRIOR FILING DATE: 1998-06-22	
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22	PRIOR APPLICATION NUMBER: 60/090355	
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24	PRIOR APPLICATION NUMBER: 60/090429	
25	PRIOR FILING DATE: 1998-06-24	
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32	PRIOR APPLICATION NUMBER: 60/090445	
33	PRIOR FILING DATE: 1998-06-24	
34	PRIOR APPLICATION NUMBER: 60/090472	
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37	PRIOR FILING DATE: 1998-06-24	
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39	PRIOR FILING DATE: 1998-06-24	
40	PRIOR APPLICATION NUMBER: 60/090542	
41	PRIOR FILING DATE: 1998-06-24	
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; PRIOR APPLICATION NUMBER: 60/092182  
; PRIOR FILING DATE: 1998-07-09

Query Match 100.0%; Score 2384; DB 9; Length 458;  
Best Local Similarity 100.0%; Pred. No. 5.4e-185;  
Matches 458; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 61 SGSCPTSHTRPCTGCTCFISLASLQWSRVSMFPTRLSPCSSATEQTERDSATAYRMTVEVL 120  
Qy 121 GTVLGTAIOGOIVGOADTPCFQDFNSSTVASOSANHTGTTSHRETOKAYLLAAGVIVCI 180  
Db 121 GTVLGTAIOGOIVGOADTPCFQDFNSSTVASOSANHTGTTSHRETOKAYLLAAGVIVCI 180  
Qy 181 YIICAVILILGVREQREPEYEAQOSEPTAYFRGLRLVMSHGPYIKLITGFLTSLAFMLVE 240  
Db 181 YIICAVILILGVREQREPEYEAQOSEPTAYFRGLRLVMSHGPYIKLITGFLTSLAFMLVE 240  
Qy 241 GNEVLFCTYTLGFRNEFQNLILAISATLTIPIWQWFLTRFGKKTAVYVGISSAVPFLI 300  
Db 241 GNEVLFCTYTLGFRNEFQNLILAISATLTIPIWQWFLTRFGKKTAVYVGISSAVPFLI 300  
Qy 301 LVALMESNLITTYAVAAAGISVAAAFLLPWSMLPDVIDDFHLKQPHFGHTEPIFFSFYV 360  
Db 301 LVALMESNLITTYAVAAAGISVAAAFLLPWSMLPDVIDDFHLKQPHFGHTEPIFFSFYV 360  
Qy 361 FFTKFAAGSVLSIGISTLSLDFAGYQTRCQSPERVKFTLNMLVTMAPIVLILGLLFLPKMY 420  
Db 361 FFTKFAAGSVLSIGISTLSLDFAGYQTRCQSPERVKFTLNMLVTMAPIVLILGLLFLPKMY 420  
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RESULT 6  
US-09-990-436-20  
; Sequence 20, Application US/09990436  
; Publication No. US20020198148A1  
; GENERAL INFORMATION:  
; APPLICANT: Ashkenazi, Avi J.  
; APPLICANT: Baker, Kevin P.  
; APPLICANT: Botstein, David  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Eaton, Dan L.

Query Match 100.0%; Score 2384; DB 9; Length 458;  
Best Local Similarity 100.0%; Pred. No. 5.4e-185;  
Matches 458; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MRLRWALSPSSCLWAEFGHPQSQTPTWASASANPPGPAWVALCPGSSPPRPWLSPTSS 60  
Db 1 MRLRWALSPSSCLWAEFGHPQSQTPTWASASANPPGPAWVALCPGSSPPRPWLSPTSS 60

Qy 61 SGSCPTSHARPICGTFCFASLKQWSRVSMPTRLSPCSSATEQTERDSATAYRTMVEVL 120  
Db 61 SGSCPTSHARPICGTFCFASLKQWSRVSMPTRLSPCSSATEQTERDSATAYRTMVEVL 120

Qy 121 GTVLGTALQGOIVGOADTPCFQDNSTVSQSANHTTGTTSRETOKAYLLAAGVIVCI 180  
Db 121 GTVLGTALQGOIVGOADTPCFQDNSTVSQSANHTTGTTSRETOKAYLLAAGVIVCI 180

Qy 181 YIICAVILILVGRQREYEAQQSEPIAYFRGLRLVMSHGPIYIKLTGFLTSLAFMLVE 240  
Db 181 YIICAVILILVGRQREYEAQQSEPIAYFRGLRLVMSHGPIYIKLTGFLTSLAFMLVE 240

Qy 241 GNFVLCFTYITGFRNEFONLLAILMSATLPIWQWELTRFGKKTAVYVGVISAVPPLI 300  
Db 241 GNFVLCFTYITGFRNEFONLLAILMSATLPIWQWELTRFGKKTAVYVGVISAVPPLI 300

Qy 301 LVALMESNLIITYAVAVAAGISVAAAFLLPWSMLPDVIDDFHLKOPFHGTEPIFFSFYV 360  
Db 301 LVALMESNLIITYAVAVAAGISVAAAFLLPWSMLPDVIDDFHLKOPFHGTEPIFFSFYV 360

Db 301 LVALMESNLIITYAVAVAAGISVAAAFLLPWSMLPDVIDDFHLKOPFHGTEPIFFSFYV 360  
Qy 361 FFTKFAAGVSLGISTLSLDFAGYQTRGCSQPERVKFTLNMLVTWAPIVLIILGLLFLPKMY 420  
Db 361 FFTKFAAGVSLGISTLSLDFAGYQTRGCSQPERVKFTLNMLVTWAPIVLIILGLLFLPKMY 420  
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Db 421 PIDERRRQNKALQALRDEASSSGCSETDSTELASIL 458

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US-09-991-181-20  
; Sequence 20, Application US/09991181  
; Publication No. US20020197615A1  
; GENERAL INFORMATION:  
; APPLICANT: Ashkenazi, Avi J.  
; APPLICANT: Baker, Kevin P.  
; APPLICANT: Botstein, David  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Eaton, Dan L.  
; APPLICANT: Ferrara, Napoleone  
; APPLICANT: Fong, Sherman  
; APPLICANT: Gerber, Hanspeter  
; APPLICANT: Gerritsen, Mary E.  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Grimaldi, J. Christopher  
; APPLICANT: Gurney, Austin L.  
; APPLICANT: Kljavin, Ivar J.  
; APPLICANT: Napier, Mary A.  
; APPLICANT: Pan, James  
; APPLICANT: Paoni, Nicholas F.  
; APPLICANT: Roy, Margaret Ann  
; APPLICANT: Stewart, Timothy A.  
; APPLICANT: Tamas, Daniel  
; APPLICANT: Watanabe, Colin K.  
; APPLICANT: Williams, P. Mickey  
; APPLICANT: Wood, William I.  
; APPLICANT: Zhang, Zemin  
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
; FILE REFERENCE: P2730PIC53  
; CURRENT FILING DATE: 2001-11-16  
; PRIOR APPLICATION NUMBER: US/09/991.181  
; PRIOR FILING DATE: 1997-06-16  
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Db 121 GTVLGTAIOGOIVQADTPCFQDFNSSTVASQSANHTGTTSHRETQKAYLLAAGVIVCI 180
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Db 241 GNFVLCFTYTLGRNRPONLLALMLSATLTIPWQWFLTRFGKKTAVYVGISSAVPFLI 300
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; Sequence 20, Application US/09993687
; Publication No. US20020198149A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
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; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
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; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2730P1C11
; CURRENT APPLICATION NUMBER: US/09/993,687
; CURRENT FILING DATE: 2002-11-14
; PRIOR APPLICATION NUMBER: 60/049787
; PRIOR FILING DATE: 1997-06-16
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APPLICANT: Tumas, Daniel  
APPLICANT: Watanabe, Colin K.  
APPLICANT: Williams, P. Mickey  
APPLICANT: Wood, William I.  
APPLICANT: Zhang, Zemin  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
TITLE OF INVENTION: Acids Encoding the Same  
FILE REFERENCE: P2730PIC84  
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PRIOR FILING DATE: 1998-06-24  
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PRIOR FILING DATE: 1998-06-24

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60/089538	PRIOR FILING DATE: 1998-06-17
60/089598	PRIOR APPLICATION NUMBER: 60/089538
60/089599	PRIOR FILING DATE: 1998-06-17
60/089600	PRIOR APPLICATION NUMBER: 60/089600
60/089653	PRIOR FILING DATE: 1998-06-17
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60/089907	PRIOR FILING DATE: 1998-06-18
60/089908	PRIOR APPLICATION NUMBER: 60/089908
60/089947	PRIOR FILING DATE: 1998-06-18
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6	PRIOR APPLICATION NUMBER:	60/090431
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27	PRIOR FILING DATE:	1998-06-25
28	PRIOR APPLICATION NUMBER:	60/090690
29	PRIOR FILING DATE:	1998-06-25
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34	PRIOR APPLICATION NUMBER:	60/090696
35	PRIOR FILING DATE:	1998-06-25
36	PRIOR APPLICATION NUMBER:	60/090862
37	PRIOR FILING DATE:	1998-06-26
38	PRIOR APPLICATION NUMBER:	60/090863
39	PRIOR FILING DATE:	1998-06-26
40	PRIOR APPLICATION NUMBER:	60/091360
41	PRIOR FILING DATE:	1998-07-01
42	PRIOR APPLICATION NUMBER:	60/091478
43	PRIOR FILING DATE:	1998-07-02
44	PRIOR APPLICATION NUMBER:	60/091544
45	PRIOR FILING DATE:	1998-07-01
46	PRIOR APPLICATION NUMBER:	60/091519
47	PRIOR FILING DATE:	1998-07-02
48	PRIOR APPLICATION NUMBER:	60/091626
49	PRIOR FILING DATE:	1998-07-02
50	PRIOR APPLICATION NUMBER:	60/091633
51	PRIOR FILING DATE:	1998-07-02
52	PRIOR APPLICATION NUMBER:	60/091978
53	PRIOR FILING DATE:	1998-07-07
54	PRIOR APPLICATION NUMBER:	60/091982
55	PRIOR FILING DATE:	1998-07-07
56	PRIOR APPLICATION NUMBER:	60/092182
57	PRIOR FILING DATE:	1998-07-09

Query Match	100.0%;	Score 2384;	DB 9;	Length 458;
Best Local Similarity	100.0%;	Pred. No. 5.4e-185;		
Matches 458;	Conservative 0;	Mismatches 0;	Indels 0;	

[illegible]

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; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/091982
; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/092182
; PRIOR FILING DATE: 1998-07-09

Query Match      100.0%; Score 2384; DB 9; Length 458;
Best Local Similarity 100.0%; Pred. No. 5.4e-185;
Matches 458; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MWLRWALSPPSSCLWAEPCMPQTPWVASASANPPGPAWVALCPGSSSPRPWPSLPTSS 60
DB 1 MWLRWALSPPSSCLWAEPCMPQTPWVASASANPPGPAWVALCPGSSSPRPWPSLPTSS 60

QY 61 SGSCPTSHTRPIGTCTFCSIASLKQWSRVSMFPRLSPCSSLATQTERDSATAYRMTVEVL 120
DB 61 SGSCPTSHTRPIGTCTFCSIASLKQWSRVSMFPRLSPCSSLATQTERDSATAYRMTVEVL 120

QY 121 GTVLGTAIOGQIVGQADTPCFQDFNSSTVASQSANHTGTTSHRETKQAYLLAAGVIVCI 180
DB 121 GTVLGTAIOGQIVGQADTPCFQDFNSSTVASQSANHTGTTSHRETKQAYLLAAGVIVCI 180

QY 181 YIICAVLILIGVREOREPEYAAQOSEPIAYFRGLRLVMSHGCPYIKLITGFLFTSLAFMLVE 240
DB 181 YIICAVLILIGVREOREPEYAAQOSEPIAYFRGLRLVMSHGCPYIKLITGFLFTSLAFMLVE 240

QY 241 GNFVLCFTYTLGRNFEQNLLAILMLSATLTIPIQWFLTRFGCKTAVYVVGISSAVPFLI 300
DB 241 GNFVLCFTYTLGRNFEQNLLAILMLSATLTIPIQWFLTRFGCKTAVYVVGISSAVPFLI 300

QY 301 LVALMESNLITTYAVAVAAGISVAAFLPLPWSMLPDVIDDFHLKQPHFGHTEPIFFSFYV 360
DB 301 LVALMESNLITTYAVAVAAGISVAAFLPLPWSMLPDVIDDFHLKQPHFGHTEPIFFSFYV 360

QY 361 FFTKFAAGVSLGISTLSLDPAGYOTRGCSOPERVKFTLNMLVTMAPVLVLILGLLFLFKMY 420
DB 361 FFTKFAAGVSLGISTLSLDPAGYOTRGCSOPERVKFTLNMLVTMAPVLVLILGLLFLFKMY 420

QY 421 PIDERRRQNKALQALRDEASSGGCSETDSTELASIL 458
DB 421 PIDERRRQNKALQALRDEASSGGCSETDSTELASIL 458

RESULT 12
US-09-990-438-20
; Sequence 20, Application US/09990438
; Publication No. US2003002754A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Kijavini, Ivar J.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic

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; PRIOR APPLICATION NUMBER: 60/090695
; PRIOR FILING DATE: 1998-06-25
; PRIOR APPLICATION NUMBER: 60/090696
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; PRIOR APPLICATION NUMBER: 60/090863
; PRIOR FILING DATE: 1998-06-26
; PRIOR APPLICATION NUMBER: 60/091360
; PRIOR FILING DATE: 1998-07-01
; PRIOR APPLICATION NUMBER: 60/091478
; PRIOR FILING DATE: 1998-07-02
; PRIOR APPLICATION NUMBER: 60/091544
; PRIOR FILING DATE: 1998-07-01
; PRIOR APPLICATION NUMBER: 60/091519
; PRIOR FILING DATE: 1998-07-02
; PRIOR APPLICATION NUMBER: 60/091626
; PRIOR FILING DATE: 1998-07-02
; PRIOR APPLICATION NUMBER: 60/091633
; PRIOR FILING DATE: 1998-07-02
; PRIOR APPLICATION NUMBER: 60/091978
; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/091982
; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/092182
; PRIOR FILING DATE: 1998-07-09

Query Match      100.0%; Score 2384; DB 9; Length 458;
Best Local Similarity 100.0%; Pred. No. 5.4e-185;
Matches 458; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1  MWLRWALSPPSSCLWAEPMSQTPWASASANPPGPAWALPCGSSSPRPWPSLPTSS 60
Db      1  MWLRWALSPPSSCLWAEPMSQTPWASASANPPGPAWALPCGSSSPRPWPSLPTSS 60
Qy      61  SGSCPTSHTRPITGTCFSTASLKQWSRVSMFPTRLSPCSSATQTERDSATAYRMTVEVL 120
Db      61  SGSCPTSHTRPITGTCFSTASLKQWSRVSMFPTRLSPCSSATQTERDSATAYRMTVEVL 120
Qy      121  GTVLGTAIQOIGVQADTCFQDFNSTVASQSANHTGTTSHRETKAYLLAAGVIVCI 180
Db      121  GTVLGTAIQOIGVQADTCFQDFNSTVASQSANHTGTTSHRETKAYLLAAGVIVCI 180
Qy      181  YIICAVILLGVREQREPEAQOSEPIAYFRGLRLVMSHGPYIKLITGFLTSLAPLVE 240
Db      181  YIICAVILLGVREQREPEAQOSEPIAYFRGLRLVMSHGPYIKLITGFLTSLAPLVE 240
Qy      241  GNFVLCFTYTLGRNEFQNLALLAIMLSATLTIPIQWFLTRFGKKTAVYVGISSAYPFLI 300
Db      241  GNFVLCFTYTLGRNEFQNLALLAIMLSATLTIPIQWFLTRFGKKTAVYVGISSAYPFLI 300
Qy      301  LVALMESNLIIITAVAVAAGISVAIAFLLPWSMLPDVIDDFHLKQPHFGHTEPIFFSFYV 360
Db      301  LVALMESNLIIITAVAVAAGISVAIAFLLPWSMLPDVIDDFHLKQPHFGHTEPIFFSFYV 360
Qy      361  FFTKFAAGSVGLSTLSLDFAGYQTRGCQPERVKFTLNMVTPMIPVILILLGLLFKMY 420
Db      361  FFTKFAAGSVGLSTLSLDFAGYQTRGCQPERVKFTLNMVTPMIPVILILLGLLFKMY 420
Qy      421  PIDERRRQNKALQALRDEASSSGCSETDSTELASIL 458
Db      421  PIDERRRQNKALQALRDEASSSGCSETDSTELASIL 458
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RESULT 13

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US-09-990-562-20
; Sequence 20, Application US/09990562
; Publication No. US20030027985A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
```

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; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2730PIC18
; CURRENT APPLICATION NUMBER: US/09/990,562
; CURRENT FILING DATE: 2001-11-14
; PRIOR APPLICATION NUMBER: 60/049787
; PRIOR FILING DATE: 1997-06-16
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/065186
; PRIOR FILING DATE: 1997-11-12
; PRIOR APPLICATION NUMBER: 60/065311
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; PRIOR APPLICATION NUMBER: 60/066770
; PRIOR FILING DATE: 1997-11-24
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Db 301 LVALMESNLITTVAVAAAGISVAAAFLPWSMLPDVIDDFHLKQPHFGHCTEIFFSFYV 360  
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Db 361 FFTKFASSVSLGISTLSLDAGYQTRGCSOPERVKFTFLNMLVTYMAPIVLILGLLFLPKMY 420  
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Db 421 PIDERRQNKALQALRDASSGCGSETDSTELASLIL 458

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US-09-997-428-20  
; Sequence 20, Application US/09997428  
; Publication No. US20030027162A1  
; GENERAL INFORMATION:  
; APPLICANT: Ashkenazi, Avi J.  
; APPLICANT: Baker, Kevin P.  
; APPLICANT: Botstein, David  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Eaton, Dan L.  
; APPLICANT: Ferrara, Napoleone  
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; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Grimaldi, J. Christopher  
; APPLICANT: Gurney, Austin L.  
; APPLICANT: Kijavlin, Ivar J.  
; APPLICANT: Napier, Mary A.  
; APPLICANT: Pan, James  
; APPLICANT: Paoni, Nicholas F.  
; APPLICANT: Roy, Margaret Ann  
; APPLICANT: Stewart, Timothy A.  
; APPLICANT: Tumas, Daniel  
; APPLICANT: Watanabe, Colin K.  
; APPLICANT: Williams, P. Mickey  
; APPLICANT: Wood, William I.  
; APPLICANT: Zhang, Zemin  
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
; FILE REFERENCE: P2730PLC44  
; CURRENT APPLICATION NUMBER: US/09/997,428  
; CURRENT FILING DATE: 2001-11-15  
; PRIOR APPLICATION NUMBER: 60/049787  
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15	PRIOR FILING DATE: 1998-06-18	
16	PRIOR APPLICATION NUMBER: 60/089907	
17	PRIOR FILING DATE: 1998-06-18	
18	PRIOR APPLICATION NUMBER: 60/089908	
19	PRIOR FILING DATE: 1998-06-18	
20	PRIOR APPLICATION NUMBER: 60/089948	
21	PRIOR FILING DATE: 1998-06-19	
22	PRIOR APPLICATION NUMBER: 60/089952	
23	PRIOR FILING DATE: 1998-06-19	
24	PRIOR APPLICATION NUMBER: 60/090254	
25	PRIOR FILING DATE: 1998-06-22	
26	PRIOR APPLICATION NUMBER: 60/090246	
27	PRIOR FILING DATE: 1998-06-22	
28	PRIOR APPLICATION NUMBER: 60/090252	
29	PRIOR FILING DATE: 1998-06-22	
30	PRIOR APPLICATION NUMBER: 60/090254	
31	PRIOR FILING DATE: 1998-06-22	
32	PRIOR APPLICATION NUMBER: 60/090349	
33	PRIOR FILING DATE: 1998-06-23	
34	PRIOR APPLICATION NUMBER: 60/090355	
35	PRIOR FILING DATE: 1998-06-23	
36	PRIOR APPLICATION NUMBER: 60/090429	
37	PRIOR FILING DATE: 1998-06-24	
38	PRIOR APPLICATION NUMBER: 60/090431	
39	PRIOR FILING DATE: 1998-06-24	
40	PRIOR APPLICATION NUMBER: 60/090435	
41	PRIOR FILING DATE: 1998-06-24	
42	PRIOR APPLICATION NUMBER: 60/090444	
43	PRIOR FILING DATE: 1998-06-24	
44	PRIOR APPLICATION NUMBER: 60/090445	
45	PRIOR FILING DATE: 1998-06-24	
46	PRIOR APPLICATION NUMBER: 60/090472	
47	PRIOR FILING DATE: 1998-06-24	
48	PRIOR APPLICATION NUMBER: 60/090535	
49	PRIOR FILING DATE: 1998-06-24	
50	PRIOR APPLICATION NUMBER: 60/090540	
51	PRIOR FILING DATE: 1998-06-24	
52	PRIOR APPLICATION NUMBER: 60/090542	
53	PRIOR FILING DATE: 1998-06-24	
54	PRIOR APPLICATION NUMBER: 60/090557	
55	PRIOR FILING DATE: 1998-06-24	
56	PRIOR APPLICATION NUMBER: 60/090676	
57	PRIOR FILING DATE: 1998-06-25	
58	PRIOR APPLICATION NUMBER: 60/090678	
59	PRIOR FILING DATE: 1998-06-25	
60	PRIOR APPLICATION NUMBER: 60/090690	
61	PRIOR FILING DATE: 1998-06-25	
62	PRIOR APPLICATION NUMBER: 60/090694	
63	PRIOR FILING DATE: 1998-06-25	
64	PRIOR APPLICATION NUMBER: 60/090695	
65	PRIOR FILING DATE: 1998-06-25	
66	PRIOR APPLICATION NUMBER: 60/090696	
67	PRIOR FILING DATE: 1998-06-25	
68	PRIOR APPLICATION NUMBER: 60/090862	
69	PRIOR FILING DATE: 1998-06-26	
70	PRIOR APPLICATION NUMBER: 60/090863	
71	PRIOR FILING DATE: 1998-06-26	
72	PRIOR APPLICATION NUMBER: 60/091360	
73	PRIOR FILING DATE: 1998-07-01	

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OM protein - protein search, using sw model

Run on: June 19, 2003, 17:44:36 ; Search time 15 Seconds  
(without alignments)  
1266.411 Million cell updates/sec

Title: US-09-941-992-20

Perfect score: 2384

Sequence: 1 MRLWALSPPSSCLWAEFG.....DEASSGCGSETDSTELASIL 458

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt\_40:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	221.5	9.3	544	1 YD74_SYNY3	P74168 synechocyst
2	153.5	6.4	463	1 GUTA_BACSU	O34368 bacillus su
3	146	6.1	479	1 XVL_P_LACPE	P96792 lactobacill
4	143.5	6.0	457	1 UDBP_ECOLI	P30868 escherichia
5	138.5	5.8	459	1 YJMB_BACSU	O34961 bacillus su
6	138	5.8	641	1 RAPP_PEDPE	P43466 pediococcus
7	133	5.6	463	1 YNAJ_BACSU	P94488 bacillus su
8	131.5	5.5	438	1 SHIA_ECOLI	P76350 escherichia
9	126.5	5.3	460	1 YAGG_ECOLI	P75683 escherichia
10	125	5.2	462	1 LACP_STAXY	O33814 staphylococ
11	112	4.7	272	1 YCR3_ERWHE	Q01334 erwinia her
12	110	4.6	485	1 YIHO_ECOLI	P32136 escherichia
13	110	4.6	1780	1 POLG_MVEV	P05769 m genome po
14	109.5	4.6	422	1 EXUT_BACSU	O34456 bacillus su
15	109	4.6	457	1 BAG4_HUMAN	O95429 homo sapien
16	106.5	4.5	1280	1 MDR1_HUMAN	P08183 homo sapien
17	106	4.4	408	1 GPT_HUMAN	O943h5 homo sapien
18	106	4.4	580	1 UAPC_EMENT	P48777 emericecia
19	105.5	4.4	512	1 MYIN_BORBU	O51750 borrelia bu
20	105	4.4	473	1 YIHO_SALTY	Q19174 salmonella
21	101.5	4.3	605	1 YIHO_YEAST	P38739 saccharomyc
22	101	4.2	476	1 MELB_SALTY	P30878 salmonella
23	101	4.2	830	1 VPP3_HUMAN	Q13488 h vacuolar
24	101	4.2	1887	1 REBL_DROME	P04052 grosophila
25	100.5	4.2	653	1 CCMF_RHOCA	Q00500 rhodobacter
26	100.5	4.2	1367	1 AMYH_YEAST	P08640 saccharomyc
27	100	4.2	415	1 CSCB_ECOLI	P30000 escherichia
28	99	4.2	408	1 GPT_CRIGR	P24140 cricetus
29	99	4.2	410	1 GPT_MOUSE	P42867 mus musculu
30	99	4.2	567	1 PROI_LEIEN	P13865 leishmania
31	98.5	4.1	284	1 CDX4_HUMAN	O14627 homo sapien
32	98.5	4.1	428	1 YXIO_BACSU	P42306 bacillus su
33	98.5	4.1	452	1 WZYE_SALTY	P37458 salmonella

34	98	4.1	408	1 GPT_CRILO	P23338 cricetus
35	98	4.1	602	1 NU5M_MACRO	P92669 macropus ro
36	97.5	4.1	452	1 WZYE_SALTY	O82396 salmonella
37	97.5	4.1	571	1 SECD_MYCLE	P38387 mycobacteri
38	97.5	4.1	658	1 CNTL_RABIT	Q9mzt2 oryctolagus
39	97	4.1	1276	1 MDR1_CRIGR	P21448 cricetus
40	96.5	4.0	461	1 YCJF_ECOLI	P76037 escherichia
41	95.5	4.0	406	1 FSR_ECOLI	P52067 escherichia
42	95.5	4.0	639	1 LACY_LEULA	Q48624 leuconostoc
43	95.5	4.0	1277	1 MDR1_RAT	P43245 rattus norv
44	95	4.0	364	1 EDG2_HUMAN	Q92633 homo sapien
45	95	4.0	448	1 Y347_CHLPP	Q928j6 chlamydia p

## ALIGNMENTS

RESULT 1					
YD74_SYNY3					
ID	YD74_SYNY3	STANDARD;	PRT;	544 AA.	
AC	P74168;				
DT	15-DEC-1998 (Rel. 37, Created)				
DT	15-DEC-1998 (Rel. 37, Last sequence update)				
DT	16-OCT-2001 (Rel. 40, Last annotation update)				
DE	Hypothetical symporter sl11374.				
GN	SL11374.				
OS	Synechocystis sp. (strain PCC 6803).				
OC	Bacteria; Cyanobacteria; Chroococcales; Synechocystis.				
OX	NCBI_taxid=1148;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RX	MEDLINE=97061201; PubMed=8905231;				
RA	Kaneko T., Sato S., Kotani H., Tanaka A., Asamizu E., Nakamura Y.,				
RA	Miyajima N., Hirotsawa M., Sugiyama M., Sasamoto S., Kimura T.,				
RA	Hosouchi T., Matsuno A., Muraki A., Nakazaki N., Naruo K., Okumura S.,				
RA	Shimpo S., Takeuchi C., Wada T., Watanabe A., Yamada M., Yasuda M.,				
RA	Tabata S.;				
RT	"Sequence analysis of the genome of the unicellular cyanobacterium				
RT	Synechocystis sp. strain PCC6803. II. Sequence determination of the				
RT	entire genome and assignment of potential protein-coding regions.";				
RL	DNA Res. 3:109-136(1996).				
CC	-  SUBCELLULAR LOCATION: Integral membrane protein (Potential).				
CC	-  SIMILARITY: BELONGS TO THE SODIUM:GALACTOSIDE SYMPORTER FAMILY				
CC	(SGF).				
CC	-----				
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CC	-----				
CC	EMBL; D90912; BAA18257.1; -				
DR	InterPro; IPR001927; Na/Gal_symp.				
DR	TIGRfam; TIGR00792; gph; 1.				
DR	PROSITE; PS00872; NA_GALACTOSIDE_SYMP; FALSE_NEG.				
KW	Hypothetical protein; Transport; Transmembrane; Symport;				
KW	Complete proteome.				
FT	TRANSMEM 31	51	POTENTIAL.		
FT	TRANSMEM 52	72	POTENTIAL.		
FT	TRANSMEM 84	104	POTENTIAL.		
FT	TRANSMEM 116	136	POTENTIAL.		
FT	TRANSMEM 162	182	POTENTIAL.		
FT	TRANSMEM 191	211	POTENTIAL.		
FT	TRANSMEM 230	250	POTENTIAL.		
FT	TRANSMEM 257	277	POTENTIAL.		
FT	TRANSMEM 318	338	POTENTIAL.		
FT	TRANSMEM 356	376	POTENTIAL.		
FT	TRANSMEM 383	403	POTENTIAL.		
FT	TRANSMEM 407	427	POTENTIAL.		
FT	TRANSMEM 450	470	POTENTIAL.		
FT	TRANSMEM 501	521	POTENTIAL.		

Db 339 FIMLFASGFTTTLNLTAWGVADCDVDAEWK-----GIRADGVWISSMSFINKGLVALA 394  
 Qy 371 LGISTLSLDAGYQTRCSCPERVKFTLNMLVMAPIV---LILGLLLFKMYPIDRER 426  
 Db 395 GSFAIYLGAGY-----VANTDQTVASNAIKNNALIPGFFILLISILLIAFTPLTEKR 449

## RESULT 3

ID XYLP\_LACPE STANDARD; PRT; 479 AA.  
 AC P96792;  
 DT 15-DEC-1998 (Rel. 37, Created)  
 DT 15-DEC-1998 (Rel. 37, Last sequence update)  
 DT 15-DEC-1998 (Rel. 37, Last annotation update)  
 DE Putative xylose-proton symporter (xylose transporter).  
 GN XYLP.  
 OS Lactobacillus pentosus.  
 OC Bacteria; Firmicutes; Lactobacillales; Lactobacillaceae;  
 OC Lactobacillus.  
 OX NCBI\_TaxID=1589;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=MD353;  
 RA MEDLINE=96233724; PubMed=9573180;  
 RA Chaillou S., Lokman B.C., Leer R.J., Posthuma C., Postma P.W.,  
 RA Pouwels P.H.;  
 CC -1- FUNCTION: RESPONSIBLE FOR TRANSPORT OF XYLOSE INTO THE CELL, WITH  
 CC THE CONCOMITANT EXPORT OF A PROTON (SYMPORT SYSTEM).  
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein (Potential).  
 CC -1- SIMILARITY: BELONGS TO THE SODIUM:GALACTOSIDE SYMPORTER FAMILY  
 CC (SGF).  
 CC -----  
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 CC -----  
 CC EMBL; U89276; AAC62250.1; -  
 CC InterPro; IPR001927; Na/Gal\_symp.  
 CC Pfam; IPR003662; sub\_transporter.  
 CC TIGRFAMs; TIGR00792; gph; 1.  
 DR PROSITE; PS00872; NA\_GALACTOSIDE\_SYMP; 1.  
 DR TRANSPORT; Sugar transport; Transmembrane; Symport.  
 FT TRANSMEM 54 74 POTENTIAL.  
 FT TRANSMEM 102 122 POTENTIAL.  
 FT TRANSMEM 131 151 POTENTIAL.  
 FT TRANSMEM 174 194 POTENTIAL.  
 FT TRANSMEM 205 225 POTENTIAL.  
 FT TRANSMEM 253 273 POTENTIAL.  
 FT TRANSMEM 289 309 POTENTIAL.  
 FT TRANSMEM 321 341 POTENTIAL.  
 FT TRANSMEM 348 368 POTENTIAL.  
 FT TRANSMEM 397 417 POTENTIAL.  
 FT TRANSMEM 431 451 POTENTIAL.  
 SQ SEQUENCE 479 AA; 52505 MW; 1555AD1084D459C7 CRC64;

Query Match 6.18; Score 146; DB 1; Length 479;  
 Best Local Similarity 20.98; Pred. No. 0.0042;  
 Matches 85; Conservative 68; Mismatches 157; Indels 96; Gaps 18;  
 Qy 76 CFSIASLKQ-----WSRVSMFTPLRLSPGSSATEQTERDSATAYRTMVE 118

Db 118 CFTVPNMSTGMKVWVAYVTYIGVDVLYSAVNIPITSILPSLTSNPQE-----RYTLS 169  
 Qy 119 VLGTVLGTATOGTGOADTPCQODFNSSTVASOSANHTGTTSHRETQKAYLLAAGVIV 178  
 Db 170 TIRQFMGT-LGATITISTIALPVAIFGSGSTSS-----AHG-----WFVVALIMA 213  
 Qy 179 CIIYICAVILITLVGREQREPEYEAQOSEPIAFYFGRGLRLVMSHGPPYIKLITGFLTSLAFML 238  
 Db 214 VIAWIFFIVFANTKERVQVQSKSIPIK--TSLKALKRNPWPWIVI--FI----- 261  
 Qy 239 VEGNFVLCFTYTLGFRNEFQ-----NLLALMISAFILTIPIWOWFTTRF 282  
 Db 262 ---NFI---YWLGMQTRSQVTYFFKYNMHDATLASFILGLQLVALLAVVITPTAKRI 314  
 Qy 283 GKKTAVYVGISSA-VPFLILVALMESLIITYAVAAAGISVAAAF--LPWSMLPDVID 339  
 Db 315 GKRNMLMGLLAIVGQLILWGGSKALNVPTITVTIGY-LGTGFVSGLIAMLAUSDV 373  
 Qy 340 DFHLKQPHFG--TEPIFFSFYVFETTFASGVSLGISTLSLDFAGYQTRGCSQPERVKFT 397  
 Db 374 YGEWK-----NGVRAEGIVTSFSSFAKFGMGICGAVTGLILSAGYVANHQAQAALN-A 428  
 Qy 398 LNMVLTMAPIV---LILLGLLLFKMYP-----DEERRQNKKAL 434  
 Db 429 IEMNVVWPIVGFGLSAIALLFYKVDKIEPKMLADLEQKHAQENAL 474

RESULT 4  
 UIDB\_ECOLI  
 ID UIDB\_ECOLI STANDARD; PRT; 457 AA.  
 AC P30868; P77457;  
 DT 01-JUL-1993 (Rel. 26, Created)  
 DT 01-NOV-1997 (Rel. 35, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE Glucuronide carrier protein (glucuronide permease).  
 GN UIDB OR GUSB OR UIDP OR Bi616.  
 OS Escherichia coli.  
 OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;  
 OC Escherichia.  
 OX NCBI\_TaxID=562;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Jefferson R.A.;  
 RL Submitted (OCT-1994) to the EMBL/GenBank/DBJ databases.  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=K12 / MG1655;  
 RX MEDLINE=97426617; PubMed=9278503;  
 RA Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,  
 RA Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,  
 RA Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,  
 RA Mau B., Shao Y.;  
 RA "The complete genome sequence of Escherichia coli K-12";  
 RL Science 277:1453-1474(1997).  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=K12;  
 RX MEDLINE=97251357; PubMed=9097039;  
 RA Aiba H., Baba T., Fujita K., Hayashi K., Inada T., Isono K.,  
 RA Itoh T., Kasai H., Kashimoto K., Kimura S., Kitakawa M.,  
 RA Kitagawa M., Makino K., Miki T., Mizobuchi K., Mori H., Mori T.,  
 RA Motomura K., Nakade S., Nakamura Y., Nishimoto H., Nishio Y.,  
 RA Oshima T., Saito N., Sampei G., Seki Y., Sivasubram S.,  
 RA Tagami H., Takeda J., Takemoto K., Takeuchi Y., Wada C.,  
 RA Yamamoto Y., Horiuchi T.;  
 RL "A 570-kb DNA sequence of the Escherichia coli K-12 genome  
 RT corresponding to the 28.0-40.1 min region on the linkage map";  
 RL DNA Res. 3:363-377(1996).  
 RN [4]  
 RP PRELIMINARY SEQUENCE OF 1-112 FROM N.A.  
 RX MEDLINE=87041472; PubMed=3534890;  
 RA Jefferson R.A., Burgess S.M., Hirsh D.;

KW Hypothetical protein; Transport; Transmembrane; Symport;  
KW Complete proteome.

FT TRANSMEM 25 45 POTENTIAL.  
FT TRANSMEM 52 72 POTENTIAL.  
FT TRANSMEM 95 115 POTENTIAL.  
FT TRANSMEM 123 143 POTENTIAL.  
FT TRANSMEM 167 187 POTENTIAL.  
FT TRANSMEM 192 212 POTENTIAL.  
FT TRANSMEM 249 269 POTENTIAL.  
FT TRANSMEM 279 299 POTENTIAL.  
FT TRANSMEM 310 330 POTENTIAL.  
FT TRANSMEM 332 352 POTENTIAL.  
FT TRANSMEM 389 409 POTENTIAL.  
FT TRANSMEM 420 440 POTENTIAL.  
SQ SEQUENCE 459 AA; 50420 MW; B807795C3276E1E3 CRC64;

Query Match 5.8%; Score 138.5; DB 1; Length 459;  
Best Local Similarity 18.9%; Pred. No. 0.013;  
Matches 63; Conservative 70; Mismatches 167; Indels 33; Gaps 8;

QY 99 SSATEQPE-RDSATAYRMVTEVLGTGLTALQGVQADTPCFQDFNSSTVASQSANHT 157  
DB 149 AMTQSEDTSTSTFRQ-TCSGALFITSV-----AVMPLLVKEDNPKV----- 192  
QY 158 HGTSTHRETOKAYLLAAGVIVCIYICAVILILGVREQREPEYEAQOSEPIAYFRGLRVM 217  
DB 193 -----GYPVVMGLFAALGVFWFYCYRNCKEKRIIIEAPK-EKLTLSVVKTFI 240  
QY 218 SHGPYIKLIGFTLTSALFMLEVGNFVLCFTYILGFNRFQNLALLMLSATLTIPTWQW 277  
DB 241 TNKPLLLVLMTIFTSISAYNIKSAMLVYFAQYNLGNVELMAYMNFIIIGSFLGVFLPK 300  
QY 278 FLTRFGKKTAVYVGISSAVPFLILVALMESNLITYAVAAAGISVAAAFLLPMSLPDV 337  
DB 301 LVKMFGRKRTAMGFGISVADLINFMLPSNVVFTILASIAFTIGIPNGIHWALVSDI 360  
QY 338 IDDFHLKOPHGHTEPIFFSYVFFTFKASGVSLGISTLSLDFAGYQTRCQSPERVKFT 397  
DB 361 IDYGEWKSQ--ERKEATTYSLEFNSRKLQSLGSLGIGLGIY-VPNAVOTAQALIG 417  
QY 398 LNMVLTWAPIVLLILGLLLEK-MYPIDEERRQ 429  
DB 418 IKALLLPALALAMFIIGFLYKLTDDQHAQ 450

## RESULT 6

ID RAP\_PDPPE STANDARD; PRT; 641 AA.  
AC P43466;  
DT 01-NOV-1995 (Rel. 32, Created)  
DT 01-NOV-1995 (Rel. 32, Last sequence update)  
DT 15-JUN-2002 (Rel. 41, Last annotation update)  
DE Raffinose carrier protein (Raffinose permease).  
GN RAFP.  
OS Pedicoccus pentosaceus.  
OC Bacteria; Firmicutes; Lactobacillales; Lactobacillaceae; Pediococcus.  
OX NCBI\_TaxID=1255;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=PPeI.0;  
RA Leenhouts K.K.J., Bolhuis A.A., Kok J.J., Venema G.G.;  
RL Submitted (XXX-1994) to the EMBL/GenBank/DBJ databases.  
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.  
CC -!- SIMILARITY: IN THE N-TERMINAL SECTION: BELONGS TO THE  
CC SODIUM:GALACTOSIDE SYMPORTER FAMILY (SGF).  
CC -!- SIMILARITY: CONTAINS 1 PTS EIIA DOMAIN.

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CC EMBL; Z32771; CAAB3664.1; -  
CC EMBL; L32093; AAA25563.1; -  
DR HSP; P20166; IGPR.  
DR InterPro; IPR001927; Na/Gal\_symp.  
DR InterPro; IPR001127; PTS\_EIIA.  
DR Pfam; PF00358; PTS\_EIIA.1; 1.  
DR ProDom; PD002243; PTS\_EIIA.1.  
DR TIGRFAMS; TIGR00792; gph; 1.  
DR TIGRFAMS; TIGR00830; pba; 1.  
DR PROSITE; PS00371; PTS\_EIIA.1; 1.  
DR PROSITE; PS00872; NA\_GALACTOSIDE\_SYMP; 1.  
KW Transmembrane; Sugar transport; Transport; Symport; Phosphorylation.  
FT DOMAIN 1 ? SGF DOMAIN.  
FT MOD\_RES 559 559 EIIA DOMAIN.  
FT TRANSMEM 25 45 PHOSPHORYLATION (BY HPR) (BY SIMILARITY).  
FT TRANSMEM 57 77 POTENTIAL.  
FT TRANSMEM 93 113 POTENTIAL.  
FT TRANSMEM 120 140 POTENTIAL.  
FT TRANSMEM 168 188 POTENTIAL.  
FT TRANSMEM 201 221 POTENTIAL.  
FT TRANSMEM 253 273 POTENTIAL.  
FT TRANSMEM 288 308 POTENTIAL.  
FT TRANSMEM 317 337 POTENTIAL.  
FT TRANSMEM 342 362 POTENTIAL.  
FT TRANSMEM 394 414 POTENTIAL.  
FT TRANSMEM 429 449 POTENTIAL.  
FT TRANSMEM 485 505 POTENTIAL.  
SQ SEQUENCE 641 AA; 69913 MW; 15BEC5F69F8C0F61 CRC64;

Query Match 5.8%; Score 138; DB 1; Length 641;

Best Local Similarity 19.8%; Pred. No. 0.021;  
Matches 73; Conservative 61; Mismatches 168; Indels 66; Gaps 13;

QY 77 FSIASLKWQSRVSMFPTRLSPCSSATEQTERDSATAYRMVTEVLGTALQGVQQA 136  
DB 138 YSPKDVGFW---SMLP-----SLTDSREREKTATFAR-----LGSTIGGLVGL 180  
QY 137 DTPCFQDFNSSTVASQSANHTGTTSHRETKAYLLAAGVIVCIYICAVILI-----L 190  
DB 181 VMPAVIFFSAKATS-----TGDNR-----GMFIFALIIICLIASANGVGL 221  
QY 191 GVREOREPEYEAQOSEPIAYFRGLRVMVSHGYPYIKLTGFTLTSALFMLEVGNFVLCFTY 250  
DB 222 GTREVDSDIRKNKQDVTGVMEIFKALAKNDQLLAAALAYLFYGVGINLSLEVYFYI 281  
QY 251 LGFRNEFQ-----NLLLAIMLSATLTIPIWQWFLTRFGKKTAVYVGISSAVPFLI-----L 301  
DB 282 MGRPKSPSILSIINIFGLI--ATSLFPV-----LSKKFSRKGVFAG--CLVFMGGIAI 332  
QY 302 VALMESNLITYAVAAAGISVAAAFLLPMSLPDVDDDFHLKOPHGHTEPIFFSFYVF 361  
DB 333 FTIAGSNLWLVLLAATMFGFPQMVFLVLMVITDSVEYQGLKLG--HRDESLSLSVRPL 390  
QY 362 FTKFASGVSLG-----ISTLSLDFAGYQTRCQSPERVKFTLNMVLTWAPIVLLILGLL 417  
DB 391 IDKFGGAINGVVQCIALISGTTGTATASSITAAGQLHFKLTMPAFPALMLIIAIGIPSK 450  
QY 418 KMYPIDEE 425  
DB 451 QIFLITEEK 458

## RESULT 7

ID YNAJ\_BACSU STANDARD; PRT; 463 AA.  
AC P94488;  
DT 15-DEC-1998 (Rel. 37, Created)  
DT 15-DEC-1998 (Rel. 37, Last sequence update)  
DT 15-JUN-2002 (Rel. 41, Last annotation update)  
DE Hypothetical symporter ynaJ.



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CC -----  
DR EMBL: M87280; AAA64975.1; .  
DR InterPro: IPR001927; Na/Gal\_symp.  
DR PROSITE: PS00872; NA\_GALACTOSIDE\_SYMP; FALSE\_NEG.  
KW Hypothetical protein.  
SQ SEQUENCE 272 AA; 29955 MW; C7C753B416F14AB6 CRC64;

Query Match 4.7%; Score 112; DB 1; Length 272;  
Best Local Similarity 22.88; Pred. No. 0.5;  
Matches 67; Conservative 41; Mismatches 122; Indels 64; Gaps 12;  
QY 167 QKAYLLAAGVIVCIYICAV-----ILILGVREQREPEYEAQSQSEIAYFGRGLRVMHSG 220  
Db 17 QHRWLCLEFGV---AYIFSVNGGLTQTLILG-----QLLRWHA 51  
QY 221 PYKILITGFLTSLAFMLVE--GNFVLCFTYITIGRNEFONLLAIIAIIATLPIPIWQWF 278  
Db 52 PPSTLTUTYMLATLPQIGSYLGAMFYVYIYLGSAFYFMWLAHILKRAAGSLAKRL 111  
QY 279 LTRFGK-----KQAVYVGISAVPF-----LILVALMESNLITTVAVAVAAGISVAAAF 327  
Db 112 TRFNKVQIFCYCAVLGVLISIALFPAPKSVFVLVPL-----TFIISTL-----YQATT 160  
QY 328 LLPWSMLPDVIDDFHLKQPHFGTEPIFFSYFFFTKFAAGVSLGISTLSLDLAFAGYOTRG 387  
Db 161 TLMWVMADVADYGENSQG--KRMDDGIIFSTFLAVLKLGMALSGAIVGWTIGFSGYV--- 215  
QY 388 CSQPERVKFVNLMLVTHAPIVILLGLLFF---KMPIDERRRQ-NKKALQAL 437  
Db 216 ANAPEQTSAMHCIVALFTVPVGLLSLAFATLRWYKLDQTMQEIINAKMQTI 269

## RESULT 12

-YIHO\_ECOLI  
ID YIHO\_ECOLI STANDARD; PRT; 485 AA.  
AC P32136; P76774;  
DT 01-OCT-1993 (Rel. 27, Created)  
DT 16-OCT-2001 (Rel. 40, Last sequence update)  
DT 16-OCT-2001 (Rel. 40, Last annotation update)  
DE Hypothetical symporter YIHO.  
GN YIHO OR B3876.  
OS Escherichia coli.  
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;  
OC Escherichia.  
OX NCBI\_TaxID=562;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=K12 / MG1655;  
RX MEDLINE=93347969; PubMed=8346018;  
RA Plunkett G. III, Burland V.D., Daniels D.L., Blattner F.R.;  
RA "Analysis of the Escherichia coli genome. III. DNA sequence of the  
RT region from 87.2 to 89.2 minutes."  
RL Nucleic Acids Res. 21:3391-3398(1993).  
RN [2]  
RP REVISIONS.  
RC STRAIN=K12 / MG1655;  
RX MEDLINE=97426617; PubMed=9278503;  
RA Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,  
RA Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,  
RA Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,  
RA Mau B., Shao Y.;  
RT "The complete genome sequence of Escherichia coli K-12."  
RL Science 277:1453-1474(1997).  
CC -1- SUBCELLULAR LOCATION: Integral membrane protein. Inner membrane  
CC (Potential).  
CC -1- SIMILARITY: BELONGS TO THE SODIUM:GALACTOSIDE SYMPORTER FAMILY  
CC (SGF).  
CC -----  
CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
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CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).

CC -----  
DR EMBL: LJ9201; AAB03009.1; ALT\_FRAME.  
DR EMBL: AE00463; AAC76873.1; ALT\_INIT.  
DR PIR: S40820; S40820.  
DR EcoGene: EGI1841; yiho.  
DR InterPro: IPR001927; Na/Gal\_symp.  
DR TIGRams: TIGR00792; gph; 1.  
DR PROSITE: PS00872; NA\_GALACTOSIDE\_SYMP; 1.  
KW Hypothetical protein; Transport; Transmembrane; Inner membrane;  
KW Symport; Complete proteome.  
FT TRANSMEM 17 37 POTENTIAL.  
FT TRANSMEM 54 74 POTENTIAL.  
FT TRANSMEM 88 108 POTENTIAL.  
FT TRANSMEM 121 141 POTENTIAL.  
FT TRANSMEM 160 180 POTENTIAL.  
FT TRANSMEM 185 205 POTENTIAL.  
FT TRANSMEM 238 258 POTENTIAL.  
FT TRANSMEM 275 295 POTENTIAL.  
FT TRANSMEM 303 323 POTENTIAL.  
FT TRANSMEM 325 345 POTENTIAL.  
FT TRANSMEM 379 399 POTENTIAL.  
FT TRANSMEM 414 434 POTENTIAL.  
SQ SEQUENCE 485 AA; 53817 MW; FB53C0CE17756500 CRC64;

Query Match 4.68; Score 110; DB 1; Length 485;  
Best Local Similarity 20.78; Pred. No. 1.3;  
Matches 82; Conservative 54; Mismatches 172; Indels 88; Gaps 15;  
QY 72 PIGTCFSA-----SLKQSRVSMFTRLSPCSSATEQTERDSATAYRMTVEVLGT 122  
Db 113 PVKTTATALFMFMFGLSYSLMNCYGAIP-----AITKNPNERAQLAAYRQGGATIGL 166  
QY 123 VLGTAIQGGIVGQADTPCFQDFNSSTVASOSANHTGTTSHRETQKAYLLAAGVIVCIYI 182  
Db 167 LICTV-----AFIPLQSLFSDSTVGACA-----ALMFSIGGF----- 199  
QY 183 ICAVILILGVREQREPEY--EAQOSEPIAYFGLVMSHGPIKLIITGFLTSLAFMLVE 240  
Db 200 ---IFMMLCYRGVKEHYVDTPPTGHKASILKSCAIFRNPLLVLICIANLCTLAFAFIKL 256  
QY 241 GNFLVFTYTLGFRNEFONLL-----LAIMLSATLTIPIWQWFLRFRGKKTAVYVVGIS 293  
Db 257 AIQVYTYQYVL---NDI-NLLSWMGFFSMGICILIGVLLVPL---TVKCFGKKQYVLAGMV 309  
QY 294 SAVPFLILVALMESNLITTVAVAVAAGISVAAAFLLPWSMLPDVIDDFHLKQPHFGH--- 350  
Db 310 LWAVGDIILNVFWGNSFTFVNFSCVAFGTAFAVNSLNWALVPTVD-----YGEWK 360  
QY 351 ----TEPIFFSYFFFTKFAAGVSLGISTLSLDLAFAGYOTRGCSQPERVKFTLNLMLVTP 406  
Db 361 TGIRAEGSVYTGTYTFFRKISAAALAGFLPGIMLTQIGY-VPNIAQSDATLOGROLIFITWP 419  
QY 407 IVL-ILGLLLLFKMPIDEER-----RRONKK 432  
Db 420 CALAIIAALTMGFFYTLNEKRFALLIEINQKNKE 455

## RESULT 13

POLG\_MVEV  
ID POLG\_MVEV STANDARD; PRT; 1780 AA.  
AC P05769;  
DT 01-NOV-1988 (Rel. 09, Created)  
DT 01-NOV-1988 (Rel. 09, Last sequence update)  
DT 16-OCT-2001 (Rel. 40, Last annotation update)  
DE Genome polypeptide [Contains: Capsid protein C (Core protein); Matrix  
DE protein (Envelope protein M); Major envelope protein E; Nonstructural  
DE proteins NS1, NS2A, and NS2B; Protease/helicase (EC 3.4.21.98) (NS3)]  
DE (Fragment).  
OS Murray valley encephalitis virus.

FT	TRANSMEM	356	376	POTENTIAL.
FT	TRANSMEM	381	401	POTENTIAL.
SEQ	SEQUENCE	422 AA;	45313 MW;	C2E291AF347F7F7EDD CRC64;
	Query Match	4.6%;	Score 109.5;	DB 1; Length 422;
	Best Local Similarity	21.9%;	Pred. No. 1.2;	Indels 123; Gaps 19;
	Matches	88;	Conservative	58; Mismatches
QY	62	GSCPTSHTRARPICTCF	SIASLKQWSRVSMFPTRL	-----SPCSATEQ-----TER 107
DB	71	GAKLTFLVAMVWYMSL	FGSAVALAFGFSLLIIRILFGMGEGPLS	ATINKMNVNWFPPPTQR 130
QY	108	DSATAYRTWTVELGTV	GLGTGTAIOGIVQADTPCFQDFNS	TVASQSANHTGHTTSHRETC 167
DB	131	ASV-----IGVNTSG	PLGGAISGPIVGM	-----AVAF-----159
QY	168	KAVLLAAGVIVCIYI	ICAVILILGVREOREPEYACQSEPIAY	PRGLRLVMHSGP-----221
DB	160	-SKWSFVLIIMIGLI	WVLWPKFVKE--KPQETIKEAP-----	AIKAETSPKEIPLTF 211
QY	222	YIKLITGFLTSLAF	MLVEGNFVLFCTYITLGFERNFQNL	-----AIMLSATLPIQWQF 278
DB	212	YLKQKT-VLFTAF	APFAY--NYLTF-----FLTWFP	SYLVDRGLSVESMSVITIPWI 263
QY	279	LRFEG-----	-----KKTAVYVGISSAVP	FLILVALMESNLIIYA--VAVAAG-----320
DB	264	LGFIGLAGAGFVS	DYVYKKTA-RKGFLSRKVVLTCLF	SSAVLIGFAGLIVATTAGAVTL 322
QY	321	ISVAAFL-----	LPWSMLPDVIDDFHLQPHFGHTEPI	FFSFVVFTRFASGVSLGIST 375
DB	323	VALSVEFLYLTG	AIYWAVIQDVVDQNV-----	GSVGMHFLA-----361
QY	376	LSLDFAGYTRGCSQ	PERVKFTLNLMLVTMAPIVLILGLL	LLF 417
DB	362	-----NTAGIIGAL	TGFIVDQTGTFSGAELLAGGLAVF	395
		STANDARD;	PRT;	457 AA.
RESULT 15	BAG4_HUMAN			
ID	BAG4_HUMAN	Q95429;	O95818;	
DT	16-OCT-2001	(Rel. 40, Created)		
DT	16-OCT-2001	(Rel. 40, Last sequence update)		
DT	15-JUN-2002	(Rel. 41, Last annotation update)		
DE	BAG-family	molecular chaperone regulator-4	(Silencer of death domains).	
DE	GN	BAG4 OR SODD.		
OS	Homo sapiens	(Human).		
OC	Eukaryota;	Metazoa;	Chordata;	Cranialata; Vertebrata; Euteleostomi;
OC	Mammalia;	Eutheria;	Primates;	Catarrhini; Homnidae; Homo.
NCBI_Taxid	9606;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RP	MEDLINE-99091615;	PubMed-9873016;		
RX	Takayama S., Xie Z., Reed J.C.;			
RT	"An evolutionarily conserved family of Hsp70/Hsc70 molecular			
RT	chaperone regulators.";			
RL	J. Biol. Chem. 274:781-786(1999).			
RN	[2]			
RP	SEQUENCE FROM N.A.			
RP	MEDLINE-99115917;	PubMed-9915703;		
RX	Jiang Y., Woronicz J.D., Liu W., Goeddel D.V.;			
RT	"Prevention of constitutive TNF receptor 1 signaling by silencer of			
RT	death domains.";			
RL	Science 283:543-546(1999).			
RN	[3]			
RP	ERRATUM.			
RA	Jiang Y., Woronicz J.D., Liu W., Goeddel D.V.;			
RL	Science 283:1852-1852(1999).			
CC	-1- FUNCTION: INHIBITS THE CHAPERONE ACTIVITY OF HSP70/HSC70 BY			
CC	PROMOTING SUBSTRATE RELEASE.			
CC	-1- SUBUNIT: BINDS TO THE ATPASE DOMAIN OF HSP70/HSC CHAPERONES.			
CC	-1- SIMILARITY: CONTAINS 1 BAG DOMAIN.			

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OM protein - protein search, using sw model

Run on: June 19, 2003, 17:45:42 ; Search time 19 Seconds  
(without alignments)  
2317.346 Million cell updates/sec

Title: US-09-941-992-20

Perfect score: 2384

Sequence: 1 MRLWALSPLPSSCLWAEFG.....DEASSGGSETDSTELASIL 458

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : PIR\_73:\*

1: pir1:\*

2: pir2:\*

3: pir3:\*

4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	308.5	12.9	487	2 AB2269	hypothetical prote
2	221.5	9.3	544	2 S75696	melibiose carrier
3	154	6.5	445	2 E97320	sugar, proton sympo
4	153.5	6.4	463	2 H69788	H+-symporter homol
5	147	6.2	514	2 H87465	sodium-galactoside
6	145	6.1	449	2 D96985	permease of the Na
7	144.5	6.1	457	2 C90919	glucuronide permaa
8	144.5	6.1	457	2 H85767	glucuronide permaa
9	143.5	6.0	457	2 B64918	glucuronide permaa
10	138.5	5.8	459	2 D69852	sodium/galactoside
11	138	5.8	641	2 S44253	raffinose carrier
12	133	5.6	463	2 A69888	H+-symporter homol
13	132.5	5.6	477	2 AC0122	Sodium,galactoside
14	131.5	5.5	438	2 G64962	shikimate transport
15	128.5	5.4	438	2 H85822	probable transport
16	127.5	5.3	438	2 B90976	shikimate transport
17	127.5	5.3	466	2 B91186	probable permaase
18	127.5	5.3	466	2 A86033	probable permaase
19	126.5	5.3	460	2 F64752	probable melibiose
20	126	5.3	463	2 D87624	sodium-galactoside
21	119	5.0	490	2 B86813	xyloside transport
22	118	4.9	458	2 B97324	sugar/Na+(H+) simp
23	117.5	4.9	1136	2 F73483	probable drug tran
24	113	4.7	457	2 AE0507	probable transport
25	113	4.7	467	2 F91228	probable permaase
26	112	4.7	272	2 S52977	hypothetical prote
27	112	4.7	317	2 S53316	mucin (clone PGM-2
28	112	4.7	469	2 E86075	probable permaase
29	112	4.7	541	2 D82302	iron(III) ABC tran

RESULT 1

AB2269

hypothetical protein alr3705 [imported] - Nostoc sp. (strain PCC 7120)

C:Species: Nostoc sp.

A:Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120

C:Date: 14-Dec-2001 #sequence\_revision 14-Dec-2001 #text\_change 30-Jun-2002

C:Accession: AB2269

R:Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Irigu

Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Tabata

DNA Res. 8, 205-213, 2001

A:Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium

A:Reference number: AB1807; MUID:21595285; PMID:11759840

A:Accession: AB2269

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-487 <KUR>

A:Cross-references: GB:BA000019; PIDN:BA075404.1; PID:g17132839; GSPDB:GN00179

A:Experimental source: strain PCC 7120

C:Genetics:

A:Gene: alr3705

Query Match 12.9%; Score 308.5; DB 2; Length 487;

Best Local Similarity 25.5%; Pred. No. 1e-15;

Matches 92; Conservative 68; Mismatches 148; Indels 53; Gaps 10;

QY 93 TRLSPCSSATEQTERDSATAYRMTVEVLGTALGTAGQIVGQADTPCFQDFNSSTVASQ 152

DB 151 TALTP-ELTQDYDERTSLNSFRFAFSIGGSILSLIL-----SKVLSL 192

QY 153 SANHTHGTTSHRETOKAYLLAGVIVICIVICAVILVGVREQREPYEA-----QOSEPI 207

DB 193 IS-----DRQQYIVLAICTVIVISVLYWCVGVREVRVLAFAEKRIQVESDSI 242

QY 208 AYFRGLRLVMSHGPIKLTIGTFLTSFLMVEGNVFLFTCTYTLGF-RNEFQNLALLAML 266

DB 243 PFEQELKIVFSNRPFVIGIVLFSMLGVIQITASIIPYFVINCMLSPESDVPPTMIAVQG 302

QY 267 SATLTTPIQWFLTRFGKKTAVYVGISSAVPFLIIVA----LMESNLIITYAVAVAGIS 322

DB 303 TALLMFLVVTALSKKIGKLVFLGMS--WIIAAAGLFLFQPGQIGLMVYMAIAGVG 359

QY 323 VAAAFLLPMSMLPDVI--DDFHLKQPHFCHGTEPIFFSVFFVFFKFAAGSVLSLSTLDF 380

DB 360 VSTAYLVPMSPMDVIELDELQTCQRR-----EGIFGFWVLLQKFGLAGFLVGNALQA 415

QY 381 AGY-----QTRGCSQPERVKFTLNMLVTMAPITVLILGLLGLLFKMYPIDEERRQNKAL 434

DB 416 SGFKEAVAGQTTLPIQPESALFAIRAVGPLPTICILFGLVLYFYFYPITREMHAEILLKL 475

QY 435 Q 435

DB 476 Q 476

hypothetical prote  
tetracycline resis  
probable permaase  
genome polypeptin  
hexuronate transp  
cation efflux syst  
tetracycline resis  
gastric mucin (clo  
cathionic amino aci  
hypothetical prote  
transport system p  
hypothetical prote  
probable amino aci  
hypothetical prote  
multidrug resistan  
transport system p

QY 138 TPCFODFNSVSAQSANHTGTTSHRETQKAYLLAAGVIVCIYIICAVILILGVREORE 197  
 Db 193 -----DQAFGQMTALIVAASIVNLFSFTVVERIQ 225  
 QY 198 PYEAQOSEPIAYRGLRLVMSHPYIKLITGFLFTSLAFMLVGNFVLCFTYTLGPRNEF 257  
 Db 226 PKRRKQ--GIRKTLISVLFKNKPLMLLISSFLAFAIGFNKILSTWVYFTYVNVHK-EF 281  
 QY 258 -----QNLLAILMSATLITPIWQWFLTRFGKKTAVYVGIS-SAVPELLILVALMESLIIT 312  
 Db 282 VFMGTVLFQGAALISNLFIP---FFSEKNGRKQVMIITAAALSISVAGLHFTPYSSIPLI 338  
 QY 313 YAVAVAAGISVAAAFLLPWSMLPDVIDDFHLKQPHFG--TEPIFFSFYVFFKFAAGVS 370  
 Db 339 FIWLEASGFPTPLNTLAWGVADCVDAEWKT----GIRADGVVSSMSFINKLGVALA 394  
 QY 371 LGTSTSLDPAGYQTRGCSOPERVKFTLNMLVMPV---LILLGLLFLKMPYIDDEER 426  
 Db 395 GSFSAYVLGIAGY---VANTDQTVASLNAIKNNALIPGFFILLISILIAFYPLTEKR 449  
 RESULT 5  
 H87465  
 sodium-galactoside symporter family protein [imported] - Caulobacter crescentus  
 C;Species: Caulobacter crescentus  
 C;Date: 20-Apr-2001 #sequence\_revision 20-Apr-2001 #text\_change 20-Apr-2001  
 C;Accession: H87465  
 R;Niernan, W.C.; Feldblyum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.; Heidelberg, J.  
 B.; Laub, M.T.; Deboy, R.T.; Dodson, R.J.; Durkin, A.S.; Gwinn, M.L.; Haft, D.H.; Kolof  
 n, J.; Ermolaeva, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C.M.  
 Proc. Natl. Acad. Sci. U.S.A. 98, 4136-4141, 2001  
 A;Title: Complete Genome Sequence of Caulobacter crescentus.  
 A;Reference number: A87249; MUID:21173698; PMID:11259647  
 A;Accession: H87465  
 A;Status: preliminary  
 A;Molecule type: DNA  
 A;Residues: 1-514 <STO>  
 A;Cross-references: GB:AE005673; NID:g13423168; PIDN:AAK23724.1; GSPDB:GN00148  
 C;Genetics:  
 A;Gene: CCL748

Query Match 6.2%; Score 147; DB 2; Length 514;  
 Best Local Similarity 22.6%; Pred. No. 0.0017;  
 Matches 79; Conservative 63; Mismatches 149; Indels 58; Gaps 14;  
 QY 146 SSTVASQSANHTGTTSHRETQKAY--LLAAGVIVCIYIIC----- 184  
 Db 169 SIYVLSQTAGVAVLSSDYQORSRYVGMWQAANYGMILVLCPLPFFITGVLKGDHDSVRA 228  
 QY 185 -----AVILILGVREOREPYEAQOSEPIAYFRGLRLVMSHPYIKLITGFLFTSLA 235  
 Db 229 MGNFIVILLPITVLLAVMTVKEAPAPPOHGKCTGLKQYWRLLMR--PSVQRL---LFADLL 283  
 QY 236 FMIVEG-----NFVLCFTYTLGF--RNEFQNLAILAIMLSATLITPIWQWFLTRFGKKTAVYV 290  
 Db 284 MGLAPGIAGTLFLFFERIKRGFDKQTQAGVLLVYVLAALAGAPLWMLAKKLGKHALVV 343  
 QY 291 GISSAVPFLIL-----VALMESNLIIYAVAVAGISVAAAFLLPWSMLPDVIDDFHLKQ 346  
 Db 344 ---AAVYAFVQVGVAMPAGSVGMGLLVLAGLPSYAAPVILVRSMMDIGDEERLES- 399  
 QY 347 HFHGTPIFFSFYVFFTKFASGVSIGIST--LSLDFAGYQTRGCSQPERVKFTLNMLVTMA 405  
 Db 400 ---GVDKTLGLIYAVITGVKLGVALAVAFIALGWGFDPK-VSTPEGDAALIGM-YAIA 454  
 QY 406 PIVILKGLLLFKMYPIDEERRQNKKAQALRDEA---SSSGCSETDS 451  
 Db 455 PAALGLVVAAMKRYPLDFAFLAEIQRL--AARDAADAASKSSAPSDS 502

RESULT 6  
 D96985

permease of the Na+, galactoside symporter family [imported] - Clostridium acetobutyli  
 C;Species: Clostridium acetobutylicum  
 C;Date: 14-Sep-2001 #sequence\_revision 14-Sep-2001 #text\_change 30-Sep-2001  
 C;Accession: D96985  
 R;Nolling, J.; Breton, G.; Omelchenko, M.V.; Markarova, K.S.; Zeng, Q.; Gibson, R.; L  
 ; Daly, M.J.; Bennett, G.N.; Koonin, E.V.; Smith, D.R.  
 J. Bacteriol. 183, 4823-4838, 2001  
 A;Title: Genome Sequence and Comparative Analysis of the Solvent-Producing Bacterium  
 A;Reference number: A96900; MUID:21359325; PMID:21359325  
 A;Accession: D96985  
 A;Status: preliminary  
 A;Molecule type: DNA  
 A;Residues: 1-449 <KUR>  
 A;Cross-references: GB:AE001437; PIDN:AAK78671.1; PID:g15023572; GSPDB:GN00168  
 A;Experimental source: Clostridium acetobutylicum ATCC824  
 C;Genetics:  
 A;Gene: CAC0694  
 C;Superfamily: melibiose carrier protein

Query Match 6.1%; Score 145; DB 2; Length 449;  
 Best Local Similarity 23.2%; Pred. No. 0.002;  
 Matches 63; Conservative 49; Mismatches 128; Indels 32; Gaps 9;  
 QY 170 YLLAAGVIVCIYIICAVILILGVREOREPYEAQOSEPIAYFRGLRLVMSHPYIKLITGF 229  
 Db 179 YPVVAGIMGLIGILSFYMTYKNTREVVAENVKKEITPKSIATVITFNALLTLILMT 238  
 QY 230 LFTSLAFMLVEGNFVLCFTYTLGFRNEFQNLAILMLS-----ATITPIWQWFLTRFG 283  
 Db 239 IFSISYNIRSSLIYVYQYNLG-----NVTLLPYINFTTIGCAVLGVSMFKLVGRFG 292  
 QY 284 KKTAVYVGISSAVPFLILVALMESNLII-----TYAVAVAAG-ISVAAAFLLPWSMLPDV 337  
 Db 293 KKRTAIG-----FLISVADSINFLPQNIYFTTILLAIGFISIPNGITWAFVSDS 346  
 QY 338 IDDFHLKQPHFGT--EPIFFSFYVFTKFAVGSLGISTLSLDFAGYQTRGCSQPERVK 395  
 Db 347 IDYGEWRT----GTRREGITYSVENFARKLAQSLAGLLSGWGLGFVGY-VANKKQSAHAL 401  
 QY 396 FTLNMLVTMAP-IVLILLGLLFLKMPYIDDEER 426  
 Db 402 FGKALLMAYPAVALLVAALIIGLLYNSDKK 433

RESULT 7  
 C90919  
 glucuronide permease [imported] - Escherichia coli (strain O157:H7, substrain RIMD 05  
 C;Species: Escherichia coli  
 C;Date: 18-Jul-2001 #sequence\_revision 18-Jul-2001 #text\_change 03-Aug-2001  
 C;Accession: C90919  
 R;Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C  
 gasawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H.  
 DNA Res. 8, 11-22, 2001  
 A;Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and 9  
 A;Reference number: A99629; MUID:21156231; PMID:11258796  
 A;Accession: C90919  
 A;Status: preliminary  
 A;Molecule type: DNA  
 A;Residues: 1-457 <HAY>  
 A;Cross-references: GB:BA000007; PIDN:BA035746.1; PID:g13361790; GSPDB:GN00154  
 A;Experimental source: strain O157:H7, substrain RIMD 0509952  
 C;Genetics:  
 A;Gene: ECS2323  
 C;Superfamily: melibiose carrier protein

Query Match 6.1%; Score 144.5; DB 2; Length 457;  
 Best Local Similarity 19.8%; Pred. No. 0.0023;  
 Matches 75; Conservative 62; Mismatches 178; Indels 63; Gaps 13;  
 QY 73 IGTCFSTASLKQWSRVSMFTRLSPCSSATEQTERDSATAYRTVVEVLGTVLGTAIQGOI 132  
 Db 119 LGLCYSLVNIPYGLSATAMTQQ--PQSRARLGAARGIAAS--LTFVCLAFILGPSIK--- 171



```
Qy 272 IPIWQFLTRFGKK-----TAVYVGISSAVPFLIILVALMESNLITITAVAVAAAGISVAAAF 327
Db 303 IPCFAWLADRGRRRVYITGLTIGLSAFFFFMALEAQSIFFWIFFSI----- 350
Qy 328 LLPWSMLPDVIDF--HLKOPHFHGPPIFFSFYVFTKFAAGVSLGISTLSLDFAGYQT 385
Db 351 -----MLANTAHDMVVCQQPMF--TE-MEGASYRY-----SGAGVGYQVASVVXGCF-- 395
Qy 386 RGCSPQPRVFTLNLMLVTM-----APIVLILGLLLFKMYPi---DEER 426
Db 396 -----TPFIAAALITYFAGNWHSVAIYLLAGCLISAMTALIMKDSQR 437

RESULT 15
H85822
probable transport protein, shikimate shia [imported] - Escherichia coli (strain O157:H7)
C:Species: Escherichia coli
C:Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 14-Sep-2001
C:Accession: H85822
R:Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhew
iller, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, K.; Apodaca,
Nature 409, 529-533, 2001
A:Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.
A:Reference number: A85480; MUID:21074935; PMID:11206551
A:Accession: H85822
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-438 <STO>
A:Cross-references: GB:AE0051174; NID:g12516157; PIDN:AAG57044.1; GSPDB:GN00145; UWGP:231
A:Experimental source: strain O157:H7, substrain EDL933
C:Genetics:
A:Gene: shia
C:Superfamily: citrate utilization determinant

Query Match 5.4%; Score 128.5; DB 2; Length 438;
Best Local Similarity 21.6%; Pred. No. 0.035;
Matches 75; Conservative 58; Mismatches 125; Indels 89; Gaps 17;

Qy 127 AIQGOIYGQADTFQDFNSSTVAS-QSANHTGCTTSHRETOKAY-----LLAAGVIVCIY 181
Db 133 AIQGFVAG-----GEMGAALLSVESAPKPKAFYSSGVQVGYGVLSTGLSVLS 185
Qy 182 I-----ICAVILILGV-----REQREPYEAOQSEPIAYFRGLRV--- 216
Db 186 MMTTDEQFLSWGRIPLFSIVLVGALWVRNGMESEAEFEQQYNOAAKKRIPVIEAL 245
Qy 217 MSH-GPIYKILITGLFTSLAPMLVEGNVLFCTYTLGRNE-FONLLLAIMLSATLPIPI 274
Db 246 LRHPGAFKIITALRCCELLTMYIVTAFALNYSQNMGLPRELFLNIGLVGLSCLTIPC 305
Qy 275 WQWFLTRFGKK---TAVYVGISSAVPFLIILVALMESNLITITAVAVAAAGISVAAAFLLP 330
Db 306 FAWXADRFGRRVYITGALIGTSAFFFFMALEAQSIFFWIFFSI----- 350
Qy 331 WSMPLPDVIDF--HLKOPHFHGPPIFFSFYVFTKFAAGVSLGISTLSLDFAGYQTRGC 388
Db 351 --MLANTAHDMVVCQQPMF--TE-MEGASYRY-----SGAGVGYQVASVVXGCF----- 395
Qy 389 SQPRVFTLNLMLVTM-----APIVLILGLLLFKMYPi---DEER 426
Db 396 -----TPFIAAALITYFAGNWHSVAIYLLAGCLISAMTALIMKDNQR 437
```

Search completed: June 19, 2003, 17:48:26  
Job time : 22 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: June 19, 2003, 17:45:17 ; Search time 35 Seconds  
(without alignments)  
2696.274 Million cell updates/sec

Title: US-09-941-992-20

Perfect score: 2384

Sequence: 1 MMLRWALSPPSCLWAEFG.....DEASSGCGSETDSTELASIL 458

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPREMBL\_21.\*

- 1: sp\_archaea.\*
- 2: sp\_bacteria.\*
- 3: sp\_fungi.\*
- 4: sp\_human.\*
- 5: sp\_invertebrate.\*
- 6: sp\_mammal.\*
- 7: sp\_mhc.\*
- 8: sp\_organelle.\*
- 9: sp\_phage.\*
- 10: sp\_plant.\*
- 11: sp\_rodent.\*
- 12: sp\_virus.\*
- 13: sp\_vertebrate.\*
- 14: sp\_unclassified.\*
- 15: sp\_rvirus.\*
- 16: sp\_bacteriap.\*
- 17: sp\_archaeap.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	1816	76.2	530	4 Q96F59	Q96f59 homo sapien
2	1807	75.8	371	4 Q9BRC8	Q9brc8 homo sapien
3	1556.5	65.3	534	11 Q9BA75	Q9ba75 mus musculus
4	308.5	12.9	487	16 Q8YQV7	Q8yqv7 anabaena sp
5	169.5	7.1	455	16 Q8R8R3	Q8r8r3 thermoaena
6	168	7.0	463	16 Q8XP13	Q8xp13 clostridium
7	154	6.5	445	16 Q97D00	Q97dq0 clostridium
8	147	6.2	514	16 Q9A7H5	Q9a7h5 caulobacter
9	145	6.1	449	16 Q97L68	Q97l68 clostridium
10	144.5	6.1	454	16 Q8XMC0	Q8xmc0 clostridium
11	144.5	6.1	457	16 Q8X673	Q8x673 escherichia
12	142	6.0	652	2 Q93RQ7	Q93rq7 lactobacill
13	132.5	5.6	477	16 Q8ZHA9	Q8zha9 yersinia pe
14	131.5	5.5	444	16 Q8ZKR3	Q8zkr3 salmonella
15	127.5	5.3	438	16 Q8X4U5	Q8x4u5 escherichia
16	127.5	5.3	466	16 Q8XDK7	Q8xdk7 escherichia

17	126	5.3	434	16 Q8R7F4	Q8r7f4 thermoanaer
18	126	5.3	463	16 Q9A413	Q9a413 caulobacter
19	125	5.2	494	2 Q9X425	Q9x425 lactococcus
20	124	5.2	494	2 Q9RAV6	Q9rav6 lactococcus
21	124	5.2	494	2 Q9RAV9	Q9rav9 lactococcus
22	122.5	5.1	489	16 Q8RIM8	Q8rim8 fusobacteri
23	121	5.1	1280	6 O46605	O46605 canis famil
24	119	5.0	490	16 Q9CFH0	Q9cfh0 lactococcus
25	118	4.9	458	16 Q97DM2	Q97dm2 clostridium
26	117.5	4.9	1136	16 Q9RWC9	Q9rwc9 deinococcus
27	113	4.7	457	16 Q8Z9N3	Q8z9n3 salmonella
28	113	4.7	467	16 Q8X8F0	Q8x8f0 escherichia
29	112.5	4.7	622	3 Q9HED4	Q9hed4 neurospora
30	112	4.7	317	6 Q29070	Q29070 sus scrofa
31	112	4.7	470	8 Q950R4	Q950r4 spizellomyc
32	112	4.7	541	16 Q9KUB4	Q9kub4 vibrio chol
33	111	4.7	374	2 P70939	P70939 bacteroides
34	111	4.7	457	16 Q8ZKZ1	Q8zrz1 salmonella
35	110.5	4.6	462	2 Q9ZB18	Q9zb18 lactococcus
36	110	4.6	386	16 Q9ZK50	Q9zk50 helicobacte
37	110	4.6	3434	12 Q9Q9F7	Q9q9f7 murray vall
38	109.5	4.6	506	17 Q8TMG4	Q8tmg4 methanosarc
39	109.5	4.6	1093	16 Q9K6B3	Q9k6b3 bacillus ha
40	109	4.6	537	10 Q8S5V1	Q8ssv1 oryza sativ
41	108.5	4.6	386	16 Q25780	Q25780 helicobacte
42	108.5	4.6	400	16 Q988C1	Q988c1 rhizobium l
43	108	4.5	528	6 Q29071	Q29071 sus scrofa
44	108	4.5	531	17 Q28500	Q28500 archaeoglob
45	107.5	4.5	387	16 Q8YU77	Q8yu77 anabaena sp

#### ALIGNMENTS

#### RESULT 1

Q96F59 ID Q96F59 PRELIMINARY; PRT; 530 AA.  
AC Q96F59;  
AT 01-DEC-2001 (TrEMBLrel. 19, Created)  
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)  
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)  
DE Similar to RIKEN cDNA I700018018 gene (Hypothetical 58.6 kDa protein).  
DE Homo sapiens (Human).  
OS Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=EYE;  
RA Strausberg R.;  
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.  
RN [2]  
RP SEQUENCE FROM N.A.  
RA Zhou X.M., Zhang P.P., Jiang H.Q., Huang Y., Qin W.X., Zhao X.T.,  
RW D.F., Gu J.R.;  
RT "Novel human cDNA clones with function of inhibiting cancer cell growth."  
RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.  
DR EMBL; BC011587; AAL11587.1; -;  
DR EMBL; AF289609; AAL55793.1; -;  
KW Hypothetical protein.  
SQ SEQUENCE 530 AA; 58623 MW; 3B6978F4EA92C763 CRC64;

Query Match 76.2%; Score 1816; DB 4; Length 530;  
Best Local Similarity 94.3%; Pred. No. 1.2e-134;  
Matches 362; Conservative 5; Mismatches 5; Indels 12; Gaps 2;  
Qy 75 TCFSIASLKQSRVSMFETRLSPCSSATQETEDRSATAYRMVTVLGTATQGOIVG 134  
!!! :!!!!!!  
Db 159 TCFHV-----YSTQETEDRSATAYRMVTVLGTATQGOIVG 206  
Qy 135 QADTPCQDFDENSSTVASQSANHTGTTSHRETQKAYLLAAGVIVCIIVILGVRE 194



```
QY 146 SSTVASQSANHTGTTSHRETQKAY--LLAAGVIVCIYIIC-----184
| | | | | : : : : : | | | : : |
Db 169 SIVVLSQTANGAVLSSDYQORSRYGWMQANVGMILVLCPPFITGVKGDHDSVRA 228
| | | | | : : : : : | | | : : |
QY 185 -----AVILILGVREOREPEYAAQSEPIAYFRGLRLVMHSGHPYKILITGFLFTSLA 235
| | | | | : : : : : | | | : : |
Db 229 MGNFIVILLPTITVLLAVMTVKEPAAPQHGKTGLKQYWRLLMR--PSVQRL--LFADLL 283
| | | | | : : : : : | | | : : |
QY 236 FMLVEG---NFVLECYITLGF--RNEFQNLALLAMLSATLTIPWQWFLTFRGKKTAVYV 290
| | | | | : : : : : | | | : : |
Db 284 MGLAPGIAGTFLFLFFFERIAGEFKTOAGVULLVYFLAALAGAPLWMLAKKLGKHKRALVY 343
| | | | | : : : : : | | | : : |
QY 291 GISSAVFLIL----VALMESNLIIITYAVAAAGISVAAAFLLPWSMLPDVIDDFHLKQP 346
| | | | | : : : : : | | | : : |
Db 344 ---AAYVAYFQVCAVMPAGSSVMGMLLVLAGLPYSAPVLRVSRMADIGDEERLES- 399
| | | | | : : : : : | | | : : |
QY 347 HFHGTETPFISFVFFTKFASGVSIGIST--LSLDFAGYQTRGCSQSPRVRFTLNMVYMA 405
| | | | | : : : : : | | | : : |
Db 400 ---GVDKTGLLYAIVTGTVKGLAVAVAFIALGWMGFDPK-VSTPEGDAALIGM-YAIA 454
| | | | | : : : : : | | | : : |
QY 406 PIVILILGLLFLFKMYPIDEERRQNKALQALRDEA---SSSGCSETDS 451
| | | | | : : : : : | | | : : |
Db 455 PAALGLVVAAMRMRYPLDRLAEIQRQL--AARDAAAADASKSAPSDDS 502
| | | | | : : : : : | | | : : |

RESULT 9
Q97L68 PRELIMINARY; PRT; 449 AA.
AC Q97L68;
DT 01-OCT-2001 (TrEMBLrel. 18, Created)
DT 01-OCT-2001 (TrEMBLrel. 18, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Permease of the Na+: galactoside symporter family.
GN CAC0694.
OS Clostridium acetobutylicum.
OC Bacteria; Firmicutes; Bacillus/Clostridium group; Clostridia;
OC Clostridiales; Clostridiaceae; Clostridium.
OX NCBI_TaxID=1488;
RN 1;
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 824 / DSM 792 / VKM B-1787;
RX MEDLINE=21359325; PubMed=11466286;
RA Noelling J., Berton G., Omelchenko M.V., Makarova K.S., Zeng Q.,
RA Gibson R., Lee H.M., Dubois J., Qiu D., Hitti J., Wolf Y.I.,
RA Tatusov R.L., Sabathe F., Doucette-Stamm L., Soucaille P., Daly M.J.,
RA Bennett G.N., Koonin E.V., Smith D.R.;
RA "Genome sequence and comparative analysis of the solvent-producing
RT bacterium Clostridium acetobutylicum.";
RL J. Bacteriol. 183:4823-4838(2001).
DR EMBL; AE007584; AAK78671.1; -
DR InterPro; IPR001927; Na/Gal_symp.
DR TIGRFAAS; TIGR00792; gph; 1.
KW Complete proteome.
SQ SEQUENCE 449 AA; 49887 MW; B447E0CF70C2C997 CRC64;

Query Match 6.1%; Score 145; DB 16; Length 449;
Best Local Similarity 23.2%; Pred. No. 0.0022;
Matches 63; Conservative 49; Mismatches 128; Indels 32; Gaps 9;

QY 170 YLLAAGVIVCIYIICAVILILGVREOREPEYAAQSEPIAYFRGLRLVMHSGHPYKILITGF 229
| | | | | : : : : : | | | : : |
Db 179 YPVVAGIMGLIGILSFYMTKYKTRVVAPAEVKNKKEITPKSIATVITFNALLTLTLMT 238
| | | | | : : : : : | | | : : |
QY 230 -LFTSLAPMLVEGNEFVLECTYTLGRNEFQNLALLAMLS-----ATLTIPWQWFLTRFG 283
| | | | | : : : : : | | | : : |
Db 239 IFSISAYNIRSSILVYVCOYNLG-----NVTLLPYINFTTICGAVLGVSFMPKLVGRFG 292
| | | | | : : : : : | | | : : |
QY 284 KKTAVYGVISSAVFLILVALMESNLII-----TYAVAAAG-ITSAVAAFLPWSMLPDV 337
| | | | | : : : : : | | | : : |
Db 293 KKRTAIG-----FLISVTAADSNFLPCNIVITFTLLAIGFISIPNGITWAFVSDS 346
| | | | | : : : : : | | | : : |
QY 338 IDDFHLKQPHFGHT--BPIFFSFYVFTKTFASGVSIGISTLSLDFAGYQTRGCSQSPRVK 395
| | | | | : : : : : | | | : : |
```

```
Db 347 IDYGEWRT---GTRREGITYSVENFARKLAQSLGSLGFLGVGY-VANKQSAHAL 401
| | | | | : : : : : | | | : : |
QY 396 FTLNMLVTMAP-IVLILGLLILFKMYPIDEER 426
| | | | | : : : : : | | | : : |
Db 402 FGKALLMAYPAVALILVLAALITGLLYNLSOKK 433
| | | | | : : : : : | | | : : |

RESULT 10
Q8XMC0 PRELIMINARY; PRT; 454 AA.
AC Q8XMC0;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Probable sugar transport protein.
GN GUTA OR CPE0769.
OS Clostridium perfringens.
OC Bacteria; Firmicutes; Bacillus/Clostridium group; Clostridia;
OC Clostridiales; Clostridiaceae; Clostridium.
OX NCBI_TaxID=1502;
RN 1;
RP SEQUENCE FROM N.A.
RC STRAIN=13 / TYPE A;
RX PubMed=11792842;
RA Shimizu T., Ohtani K., Hirakawa H., Ohshima K., Yamashita A.,
RA Shiba T., Ogasawara N., Hattori M., Kuhara S., Hayashi H.;
RT "Complete genome sequence of Clostridium perfringens, an anaerobic
RT flesh-eater.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:996-1001(2002).
DR EMBL; AP003188; BAB80475.1; -
DR InterPro; IPR001927; Na/Gal_symp.
DR TIGRFAAS; TIGR00792; gph; 1.
KW Sugar transport; Complete proteome.
SQ SEQUENCE 454 AA; 49661 MW; 9EDB58F22755A90E CRC64;

Query Match 6.1%; Score 144.5; DB 16; Length 454;
Best Local Similarity 20.9%; Pred. No. 0.0024;
Matches 64; Conservative 65; Mismatches 138; Indels 39; Gaps 11;

QY 146 SSTVASQSANHTGTTSHRETQKAYL-----LAAGVIVCIYIICA 185
| | | | | : : : : : | | | : : |
Db 143 SANITRSSGKTKIVTSARTV--AYGVNFIILTSTPLVSTIGNQWTVAIIVCFATIFT 200
| | | | | : : : : : | | | : : |
QY 186 VILILGVREOREPEYAAQSEPIAYFRGLRLVMHSGHPYKILITGFLTSLAPMLVEGNEVL 245
| | | | | : : : : : | | | : : |
Db 201 WYTFAGIREIKDNV-AKKKEQKQKQFINLKTWKPLRIVLLSMLVLELSSIKNTISY 259
| | | | | : : : : : | | | : : |
QY 246 FCTYTLGRNEFQ-NLLAIAMLSATLTIPWQWFLT-RFGKKTAVYVGI--SSAVPFIL 301
| | | | | : : : : : | | | : : |
Db 260 YVKY--NFNAEMMIPVYSSVGMGASILGGIMSPFLTKLGRKNTALLGLAGAAGSFLV 317
| | | | | : : : : : | | | : : |
QY 302 VALMESNLIIITYAVAAAGISVAAAFLLPWSMLPDVIDDFHLKQPHFGHTGTFPFVVF 361
| | | | | : : : : : | | | : : |
Db 318 L-LSYSSLPLMIVINFTGIPDGAGYITLTSWADCEVGEWKTG--KRSEGMIFSLNIF 374
| | | | | : : : : : | | | : : |
QY 362 FTTFASGVSLGISTLSLDFAGYQTRGCSQSPRVRFTLN---MLVTMAPIVILILGLLFLK 418
| | | | | : : : : : | | | : : |
Db 375 KSKTASAGSGLCYIAYIGY----TANESQSAFTLNGIHLIOTLTPCAIVILSFILLR 430
| | | | | : : : : : | | | : : |
QY 419 MYPIDE 424
| | | | | : : : : : | | | : : |
Db 431 RYNLSE 436
| | | | | : : : : : | | | : : |

RESULT 11
Q8X673 PRELIMINARY; PRT; 457 AA.
AC Q8X673;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Glucuronide permease.
```

OC Yersinia.  
OX NCBI\_TaxID=632;  
RN [1]  
RC STRAIN=CO-92 / BIOVAR ORIENTALIS;  
RP MEDLINE=21470413; PubMed=11586360;  
RX Parkhill J., Wren B.W., Thomson N.R., Titball R.W., Holden M.T.G.,  
RA Prentice M.B., Sebahia M., James K.D., Churcher C., Mungall K.L.,  
RA Baker S., Basham D., Bentley S.D., Brooks K., Cerdano-Tarraga A.M.,  
RA Chillingworth T., Cronin A., Davies R.M., Davis P., Dougan G.,  
RA Feltwell T., Hamlin N., Holroyd S., Jagels K., Karlyshev A.V.,  
RA Leather S., Moule S., Oyston P.C.F., Quail M., Rutherford K.,  
RA Simmonds M., Skelton J., Stevens K., Whitehead S., Barrell B.G.;  
RT "Genome sequence of Yersinia pestis, the causative agent of plague.";  
RL Nature 413:523-527(2001).  
DR EMBL; AJ414145; CAC89838.1; -;  
DR InterPro; IPR001927; Na/Gal\_symp.  
DR TIGRFAMs; TIGR00792; gph; 1.  
KW Complete proteome.  
SQ SEQUENCE 477 AA; 53203 MW; 66643207E7686DAF CRC64;  
  
Query Match 5.6%; Score 132.5; DB 16; Length 477;  
Best Local Similarity 18.7%; Pred. No. 0.022;  
Matches 73; Conservative 78; Mismatches 155; Indels 85; Gaps 15;  
  
Qy 74 GTCFSIASLKOWSRVSMFTRLSPCSSATEQTERDSATAYRMTVEVLGTGTAIQGIV 133  
Db ||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : :  
147 GTLVASDIPW-----SMTVMTDEPQERAKTATCATMLGVNAG-----I 186  
  
Qy 134 GOADTPCFQDFNSSTVASQSANTHTGTSRETOKAYLLAAGVICIYICAVLILGVR 193  
Db ||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : :  
187 GA--TMILFPYISGLFAENSAD-----RGYF--AGVVI--LMVLGVILMLNGFF 229  
  
Qy 194 EOREPYEAQOSEPAYRGLRLVMSHGPIKLTIGELFTSLAFLMVEGNVFLCTYTLGF 253  
Db ||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : :  
230 NTKERVNVYTEKVTLKQTFIVWQNKPLFILLSAF--FMNVFSNIVNTYIFFFTYNMG- 287  
  
Qy 254 RNEFQNLALLAMLSATLTIPIWQWFLTRFGCKTAYV-----GISSAVP 297  
Db ||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : :  
288 DAELVSVGLITFTCALAC-LGTFPLTRHFKKRLDFTLCVLEIARVGFNFTGYNVVS 346  
  
Qy 298 FLIIVALMESNLIIYAVAVAGISVAAFLPWSMLPDVIDDFHLKOPFHGTE---PI 354  
Db ||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : :  
347 VMWVLTITAIFFMNTNLISA-----MIADTVE-----YSYHTGKRCAAI 387  
  
Qy 355 FFSYVFFTFKASVGLISLTLDFAGYQTRGCSQPERVKFTLNL---VTMAPIVLIL 411  
Db ||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : :  
388 TFSQGTQVGLSVAVAGVSGSLISLILGYMPNVAQS-----TWLNLGFFCISLLPVGAV 443  
  
Qy 412 LGLLFLKMPIDERRRQNKALQALRDEAS 442  
Db ||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : :  
444 VRILMKRYKTEDEHAILREELAQGRFHSS 474  
  
RESULT 14  
Q8ZKR3  
ID Q8ZKR3 PRELIMINARY; PRT; 444 AA.  
AC Q8ZKR3;  
DT 01-MAR-2002 (TrEMBLrel. 20, Created)  
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)  
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)  
DE Putative permease of the Na<sup>+</sup>/galactoside symporter family.  
GN STW4065.  
OS Salmonella typhimurium.  
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;  
OX NCBI\_TaxID=602;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=LT2 / SGSC1412 / ATCC 700720;  
RX MEDLINE=21534948; PubMed=11677609;  
RA McClelland M., Sanderson K.E., Spieth J., Clifton S.W., Latreille P.,  
RA Courtney L., Porwollik S., Ali J., Dante M., Du F., Hou S., Layman D.,

RA Leonard S., Nguyen C., Scott K., Holmes A., Grewal N., Mulvaney E.,  
RA Ryan E., Sun H., Florea L., Miller W., Stoneking T., Nhan M.,  
RA Waterston R., Wilson R.K.;  
RT "Complete genome sequence of Salmonella enterica serovar Typhimurium  
LT2.";  
RL Nature 413:852-856(2001).  
DR EMBL; AE008890; AAL22905.1; -;  
DR InterPro; IPR001927; Na/Gal\_symp.  
DR TIGRFAMs; TIGR00792; gph; 1.  
KW Hypothetical protein; Complete proteome  
SQ SEQUENCE 444 AA; 49680 MW; A0E68PFD55C60700E CRC64;  
  
Query Match 5.5%; Score 131.5; DB 16; Length 444;  
Best Local Similarity 19.8%; Pred. No. 0.025;  
Matches 69; Conservative 60; Mismatches 160; Indels 59; Gaps 10;  
  
Qy 102 TEQTERDSATAYRMTVEVLGTGTAIQGQI---VGQADTPCFQDFNSSTVASQSANTHT 158  
Db ||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : :  
136 SDPVERLSANGYRFVMTKIAAFLTVVPMVLAVMLGQGNKALGYQFSMLGMGAMGA---- 191  
  
Qy 159 GTTSHRETQKAYLLAAGVICIYICAVILILGVREQREPYEAQOSEPIAYRGLRLVMS 218  
Db ||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : :  
192 -----LIFIFC-----FLTTRERSEP-----EITSLSVKGOKFYLLR 223  
  
Qy 219 HGPYIKLTGFTSLAFLMVEGNVFLCTYTLGFRNEFQNLALLAMLSATLTIPIWQWFL 278  
Db ||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : :  
224 NDQWILGVVILLMCGVIRGSAVAAKYKYLNGGDSLSPFLTGTGVSILAMIAITW 283  
  
Qy 279 LTRFGKKTAVYVGISSAVPFLILVLM-----ESNLIIYAVAVAGISVAAFLPWSM 333  
Db ||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : :  
284 ITKFWDKIKMP-RYTQIITF-ILSALMVFSYGRNVLAFAYFLINFFCDQMOPVFWSS 341  
  
Qy 334 LPVDVDDFHLKOPFHGTEP-----IFFSYVFFTFKASVGLISLTLDFAGYQTR 386  
Db ||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : :  
342 IAEAVD-----YGEKTKLGRVSLGFLAFGLIFQFGMGAGIAGLGLFLLSHFGYQA- 391  
  
Qy 387 GCSQPERVKFTLNLVMTAPIVLILGLLFLKMPIDERRRQNKAL 434  
Db ||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : :  
392 DVEQSARSLTGIALMNTLIPALFHLAVGLMLKKYLLINNEYRDIQAL 439  
  
RESULT 15  
Q8X4U5  
ID Q8X4U5 PRELIMINARY; PRT; 438 AA.  
AC Q8X4U5;  
DT 01-MAR-2002 (TrEMBLrel. 20, Created)  
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)  
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)  
DE Putative transport protein, shikimate.  
GN SHIA OR Z3138 OR ECS2778.  
OS Escherichia coli O157:H7.  
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;  
OX NCBI\_TaxID=83334;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=O157:H7 / EDL933 / ATCC 700927;  
RX MEDLINE=21074935; PubMed=11208551;  
RA Perna N.T., Plunkett G. III, Burland V., Mau B., Glasner J.D.,  
RA Rose D.J., Mayhew G.F., Evans P.S., Gregor J., Kirkpatrick H.A.,  
RA Posfai G., Hackett J., Klink S., Boutin A., Shao Y., Miller L.,  
RA Grobbeck E.J., Davis N.W., Lim A., Dimalanta E.T., Potamousis K.,  
RA Apodaca J., Anantharaman T.S., Lin J., Yen G., Schwartz D.C.,  
RA Welch R.A., Blattner F.R.;  
RT "Genome sequence of enterohaemorrhagic Escherichia coli O157:H7";  
RL Nature 409:529-533(2001).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC STRAIN=O157:H7 / RIMD 0509952;  
RX MEDLINE=21156231; PubMed=11258796;  
RA Hayashi T., Makino K., Ohnishi M., Kurokawa K., Ishii K., Yokoyama K.,  
RA Han C.-G., Ohtsubo E., Nakayama K., Murata T., Tanaka M., Tobe T.,  
RA Iida T., Takami H., Honda T., Sasakawa C., Ogasawara N., Yasunaga T.,